

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTtACCAATGATTGCCCTAACTCGAGTA
1	DK7	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTcACCAATGATTGCCCTAACTCGAGTA
8	US11	1 TACCAAGTaCGCAACTCCACGGGGCTTTACCATGTcACCAATGATTGCCCTAACTCGAGTA
4	DR4	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTcACCAATGATTGCCCTAATTTCGAGTA
3	DR1	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTcACCAATGATTGCCCTAATTTCGAGTA
2	DK9	1 TACCAAGTACGCAACTCCtCGGGCCTcTACCATGTcACCAATGATTGCCCTAACTCGAGTA
6	S18	1 TACCAAGTACGCAACTCCaCGGGCCTTTACCATGTcACCAATGAcTGCCCTAACTCGAGcA
7	SW1	1 TACCAAGTACGCAACTCCtCGGGCCTTTACCATGTcACCAATGAcTGCCCTAACTCGAGtA
1-8	consensus	tACCAAGT - CGCAACTCcaCgGGGcCTtTACCATGTcACCAATGAcTGCCCTAAcTCGAGtA

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	62 TtGTGTACGAGaCaGcTcGATGcTATCCTaCACgCTCCGGGaTGTGTCCCTTGCGTTcGtGA
1	DK7	62 TcGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTCCCTTGCGTTcGCGA
8	US11	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTcCCTTGCGTTcGCGA
4	DR4	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACAGCCGGGGTGTGTCCCTTGCGTTcGCGA
3	DR1	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACgCGCCGGGGTGTGTCCCTTGCGTTcGCGA
2	DK9	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCATtTCTCCaGGGTGTGTCCCTTGCGTTcGCGA
6	S18	62 TTGTGTACGAGACGGCCGATaCCATcCTACACTCTCCgGGGTGTGTCCCTTGCGTTcGCGA
7	SW1	62 TTGTGTACGAGACGGCCGATgCCATtCTACACTCTCCaGGGTGTGTCCCTTGCGTTcGCGA
1-8	consensus	TtGTGTACGAGgCgGCCGATgCcATcCTgCAC - CtCCgGGgTGTGTcCCTTGCGTTcGcGA

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	123 GGGTAACacCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGAcGGCAAA
1	DK7	123 GGGTAACGtCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGAtGGCAAA
8	US11	123 GGGTAACGcTTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
4	DR4	123 GGGTAACaCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
3	DR1	123 GGGTAACGCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
2	DK9	123 GGGTAACGCCTCGAaATGTTGGGTGGCGGTGGCCCCACGGTGGCCACCAGGGACGGCAAg
6	S18	123 GGGTAACGCCTCGAgATGTTGGGTGcCGGTGGCCCCACAGTtGCCACCAGGGACGGCAAA
7	SW1	23 GGATggCGCCcCGAagTGTTGGGTGgCGGTGGCCCCACAGTcGCCAcTAGGGACGGCAAA
1-8	consensus	GGgTaaCgcctCGAggTGTTGGGTGgCGgTGaCCCCACgGTgGCCACcAGGGAcGGCAaa

FIGURE 1A

SEQ ID NO:	Isolate	Sequence
5	S14	184 CTCCCCgCAaCGCAGCTTCGACGTtACATCGATCTGCTtGTCGGGAGcGCCACCCTCTGTT
1	DK7	184 CTCCCCACAgCGCAGCTTCGACGTcACATCGATCTGCTcGTCGGGAGtGCCACCCTCTGTT
8	US11	184 CTCCCCACAACGCAaCTTCGACGTcACATCGATCTGCTTGTcGGGAGCGCCACCCTCTGTT
4	DR4	184 CTCCCCACAACGcAGCTcCGACGTcACATCGACCTGCTTGTcGGGAGCGCCACCCTCTGCT
3	DR1	184 CTCCCCACAACGcAGCTTCGACGTcACATCGACCTGCTTGTcGGGAGCGCCACCCTCTGCT
2	DK9	184 CTCCCCGCAACGcAGCTTCGACGTcACATCGATCTGCTTGTcGGGAGCGCCACCCTCTGCT
6	S18	184 CTCCCCGCAACGcAGCTTCGACGTcACATCGATCTGCTTGTtGGGAGCGCCACCCTCTGCT
7	SW1	184 CTCCcTtGCAACGcAGCTTCGACGTcACATCGATCTGCTTGTtGGaAGCGCCACCCTCTGCT
1-8	consensus	CTCCCCc - CAaCGCAgCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCCTCTGcT

SEQ ID NO:	Isolate	Sequence
5	S14	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTTCTTGTcGGTCAgCTGTTTACCTT
1	DK7	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTcGGTCAACTGTTTACCTT
8	S11	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTcGGTCAACTGTTTACCTT
4	DR4	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTCTTGTcGGTCAACTGTTcACCTT
3	DR1	245 CGGCCCTCTACGTGGGGGACcTGTGCGGGTCTGTCTTCTTGTcGGTCAACTGTTcACCTT
2	DK9	245 CGGCCCTCTATGTGGGGGACtTGTGCGGGTCTGTCTTCTTGTcGGCCAACTGTTcACCTT
6	S18	245 CGGCCCTCTATGTGGGGGACcTGTGCGGGTCTGTCTTTCTTGTcAGCCAgCTGTTCACTaT
7	SW1	245 CGGCCCTCTAcGTGGGGGACtTGTGCGGGTCTGTCTTTCTcGTCAGtCAaCTGTTcACgtT
1-8	consensus	CGGCCCTCTAcGTGGGGGAC - TGTGCGGGTCTGTCTTtCTtGTCgGtCAaCTGTTcACctT

SEQ ID NO:	Isolate	Sequence
5	S14	306 CTCTCCCAGGCGCctCTGGACGACGCAAGaCTGCAATTGTTCTATCTATCCcGGCCATATA
1	DK7	306 CTCTCCCAGGCGCCACTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCtGGCCATATA
8	S11	306 CTCTCCCAGaCGCCACTGGACGACGCAgGGCTGCAATTGTTCTATCTATCCCGGCCATATA
4	DR4	306 CTCTCCCAGGCaCCACTGGACAACGCAAGACTGCAATTGTTcATCTATCCCGGCCATATA
3	DR1	306 tTCTCCCAGGCGCCACTGGACAACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
2	DK9	306 CTCCCCAGaCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTATCCCCGGCCATAt
6	S18	306 CTCCCCAGGCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTATCCCCGGCCATATA
7	SW1	306 CTCCCCAGGCGCCACTGGACAACGCAAGACTGtAACTGTTCTATCTAtCCCCGGCCAcATA
1-8	consensus	cTCTcCCCAGgCgCCaCTGGACaACGCAaGaCTGcAAtTGTTCTAtCTAtCCcGGCCAtAta

FIGURE 1A

SEQ ID NO:	Isolate	
5	S14	367 ACGGGTCatCGCATGGCaTGGGATATGATGATGAACTGGTCCCCTACgACGGCaCTGGTAG
1	DK7	367 ACGGGTCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCTACcACGGCGTTGGTAG
8	S11	367 ACGGGTCACCGCATGGCaTGGGATATGATGATGAACTGGTCCCCTACGgCGGCGTTGGTgG
4	DR4	367 ACGGGcCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCTACGACAGCGCTGGTAG
3	DR1	367 ACGGGaCACCGtATGGCaTGGGATATGATGATGAACTGGTCCCCTACGACAGCGCTGGTAA
2	DK9	367 ACGGGTCatCGcATGGCgTGGGATATGATGATGAACTGGTCCCCTACAgCAGCGCTGGTAA
6	S18	367 ACGGGTCACCGtATGGCATGGGATATGATGATGAACTGGTCCCCTACAACgGCGtTGGTAA
7	SW1	367 ACGGGTCACCGcATGGCATGGGATATGATGATGAACTGGTCCCCcACAACaGCGcTGGTAG
1-8	consensus	ACGGGtCAcCGcATGGCaTGGGATATGATGATGAACTGGTCCCCTACgaC-GCgcTGGTag

SEQ ID NO:	Isolate	
5	S14	428 TAGCTCAGCTGCTCCGGATCCCcCAAGCCATCTTGGATATGATCGCTGGTGTCTACTGGGG
1	DK7	428 TAGCTCAGCTGCTCCGGATCCCgCAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
8	S11	428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGaGCCCACTGGGG
2	DK9	428 TGGCgCAGCTGCTCAGGATCCCGCAgGCCATCTTGGACATGATCGCTGGTGTCTACTGGGG
6	S18	428 TAGCTCAGCTGCTCAGGgTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGTCTACTGGGG
7	SW1	428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGTCTACTGGGG
1-8	consensus	TaGCTcAGCTGCTCcGGATCCC-CAaGCCaTCTTGGACATGATCGCTGGtGCcCACTGGGG

SEQ ID NO:	Isolate	
5	S14	489 AGTCCTaGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCCTaGtgGTG
1	DK7	489 AGTCCTgGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCCTGGTAGTG
8	S11	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCCTGGTAGTG
4	DR4	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCCTGGTAGTG
3	DR1	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCGTGGTAGTG
2	DK9	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGgAACTGGGCGAAGGTCGTGGTgGTa
6	S18	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGcGGGgAACTGGGCGAAGGTCCTGcTAGTG
7	SW1	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGtGGGgAACTGGGCGAAGGTCCTGaTAGTG
1-8	consensus	AGTCCTaGCGGGCATAGCGTATTTtTCCATGGtGGGgAACTGGGCGAAGGTCcTggTaGTg

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	550 CTGCTGCTATTcGCCGGCGTtGACGCG
1	DK7	550 CTGCTGCTATTTGCCGGCGTCGACGCG
8	US11	550 CTGCTGCTATTTGCCGGCGTCGACGCG
4	DR4	550 CTGTTGCTGTTTGCCGGCGTTGATGCG
3	DR1	550 CTGTTGCTGTTTGCCGGCGTTGATGCG
2	DK9	550 CTGTTGCTGTTTaCCGGCGTCGATGCG
6	S18	550 CTGTTGCTGTTTgCCGGCGTCGATGCG
7	SW1	550 CTGTTGCTGTTTtCCGGCGTCGATGCG
1-8	consensus	CTGtTGCTgTTtgCCGGCGTcGAtGCG

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	1 TATGAAGTGC GCAACGTGTCCGGGgTGTACCAcGTCACaAACGACTGCTCCAACtCAAGCA
24	T10	1 TATGAAGTGC GCAACGTGTCCGGGaTGTACCAcGTCACgAACGACTGCTCCAACtCAAGCA
10	D3	1 TATGAAGTGC GCAACGTGTCCGGGGTGTACCAaGTCACcAaTGA CTGTTCCAACtCGAGCA
9	D1	1 TATGAAGTGC GCAACGTGTCCGGGGTGTACCAcGTCACGAACGACTGTTCCAACtCGAGCA
14	HK5	1 TATGAAGTGC GCAACGTGTCCGGGGTATACCAcGTCACGAACGACTGCTCCAACtCAAGCA
15	HK8	1 TATGAAGTGC GCAACGTGTCCGGGATATACCAcGTCACGAACGACTGCTCCAACtCAAGCA
12	HK3	1 TATGAAGTGC GCAACGTGTCCGGGATATACCAcGTCACGAACGACTGCTCCAACtCAAGCg
23	T3	1 TAcGAAGTGC GCAACGTGTCCGGGGTGTACcATGTCACGAACGACTGTTCCAACtCAAGCA
22	SW2	1 TATGAAGTGC GCAACGTGTCCGGGGTGTAcCATGTCACGAACGACTGTTCCAACtCAAGCA
17	IND8	1 TATGAgGTGC GCAACGTGTCCGGGGTGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
16	IND5	1 TATGAAGTGC GCAACGTGTCCGGGGTGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
21	SA10	1 TATGAAGTGC GCAACGTGTCCGGGaTGTACCAcGTCACGAACGACTGCTCCAACtCAAGCA
20	S45	1 TATGAAGTGC GCAACGTGTCCGGGgcGTACCAcGTCACGAACGACTGCTCCAACtCAAGCA
25	US6	1 TATGAAGTGC GCAACGTGTCCGGGATGTACCAcGTCACGAACGACTGCTCCAACtCAAGCA
13	HK4	1 cATGAAGTGCaCAACGTaTCCGGGATcTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
18	P10	1 TATGAAGTGC GCAACGTgTCCGGGGTGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
19	S9	1 TATGAAGTGC GCAACGTaTCCGGGGcGTACCAcGTCACGAACGACTGCTCCAACtCAAGTA
9-25	consensus	tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACgAAcGACTGcTCCAACtcaAGca

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	62 TcGTGTaTGAGGCAGtGGACgTGATCATGCAtACCCCaGGGTGCGTGCCCTGCGTTCGGGA
24	T10	62 TtGTGTtTGAGGCAGCGGACtTGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
10	D3	62 TcGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
9	D1	62 TtGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
14	HK5	62 TCGTGTAcGAGACAaCGGACATGATCATGCACACCCCTGGGTGCGTGCCCTGCGTTCGGGA
15	HK8	62 TCGTGTATGAaACAGCGGACATGATtATGCATACCCCTGGATGCaTGCCCTGCGTTCGGGA
12	HK3	62 TCGTGTATGAGACAGCaGACATGATCATGCATACCCCTGGATGCGTGCCCTGCGTaCGGGA
23	T3	62 TTGTGTATGAGACAGCGGACATGATCATGCACaACCCCTGGGTGCGTGCCCTGCGTTCGGGA
22	SW2	62 TTGTGTATGAGACAGCGGACATGATCATGCAtACCCCGGGTGCGTGCCCTGCGTTCGGGA
17	IND8	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
16	IND5	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGCGTTCGGGA
21	SA10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGA
20	S45	62 TTGTGTATGAGGCAGtGGACgTGATCtTGACACCCCTGGGTGCGTGCCCTGCGTTCGGGA
25	US6	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGtGTTCGGGA
13	HK4	62 TTGTGTATGAGGCAGCGGACATGATCATGCAtACCCCGGGTGCGTGCCCTGcGTcCGGGA
18	P10	62 TTGTGTATGAGGCAGCGGACATGATaATGCACACCCCGGGTGCGTGCCCTGtGTTCGGGA
19	S9	62 TTGTGTAcGAGGCAGCGGACgTGATcATGCAtACCCCGGGTGtGTaCCCTGcGTTCaGGA
9-25	consensus	TtGTGTatGAggCAgcgGACaTGATcaTGCAcACcCCcGGgTGcgTgCCCTGcGTtCcGGA

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	123 GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCACcCCCACGCTCGCGGCCAGGAACgCCAGC
24	T10	123 GGgCAACTCCTCCCGCTGCTGGGTAGCGCTCActCCCACGCTCGCGGCCAGGAACACCAGC
10	D3	123 GGACAACTCCTCTCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAATAGCAGC
9	D1	123 GGACAACTCCTCTCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAATGGCAaC
14	HK5	123 aAACAACTCCTCCCGTTGtTGGGTAGCGCTCgCCCCACGCTCGCGGCcAGGAACgCcCAGC
15	HK8	123 GAACAACTCCTCCCGTTGcTGGGTgGCGCTCACTCCCACGCTCGCGGctAGGAATGTCAGC
12	HK3	123 GAACAACTCCTCCCGCTGtTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGTCAGC
23	T3	123 GAgCAAtTCCTCCCGCTGCTGGGTAGCGCTtACTCCCACGCTCGCGGCCAGGAACGCCAGC
22	SW2	123 GGcCAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTaGCaGCCAGGAACaCCAGC
17	IND8	123 GGGCAACTtCTCTaGtTGCTGGGTAGCGCTCACTCCCCTCTCGCGGctAGGAACGCCAGC
16	IND5	123 GGGCAACTCCTCTCGCTGCTGGGTAGCGCTCACTCCCCTCTCGCGGCCAGGAACGCCAGC
21	SA10	123 GAACAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAActCCAGC
20	S45	123 GAACAACTCCTCCCGtTGCTGGGTgGCGCTCACTCCCACGCTCGCGGCCAGGAActCCAGC
25	US6	123 GAACAAtTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGctAGC
13	HK4	123 GAACAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCCAGC
18	P10	123 GAACAACTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACaCTCGCGGctAGGAAttCCAGC
19	S9	123 GggtAACTCCTCCCaTGCTGGGTgGCGCTCACcCCCACgCTCGCGGCcAGGAACgCtAcc
9-25	consensus	gaacAActcCTCccgcTGcTGGGTaGCGCTcaCtCCCACgCTcGCgGCcAGGAACgcccAgC

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	184 aTCCCCACTACGACaATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
24	T10	184 GTCCCCACTACGACgATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
10	D3	184 GTCCCCACTACGACaATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
9	D1	184 GTCCCCACTACGGCgATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
14	HK5	184 GTCCCCACcACGGCAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
15	HK8	184 GTCCCCACtACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
12	HK3	184 GTCCCCACcACGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGcTTCTGCT
23	T3	184 GTCCCCACTAaGACAATACGACGTCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGtT
22	SW2	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGcT
17	IND8	184 GTCCCCACCACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGTT
16	IND5	184 GTCtCCACCACGACAATACGACaCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGTT
21	SA10	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
20	S45	184 GTCCCCACTACGACAATACGACGtCACGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
25	US6	184 GTCCCCACTACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTaCTTTCTGCT
13	HK4	184 aTCCCCACTACGACAATACGACGCCATGTCGAcTTGCTCGTTGGGGCGGCTGCTTTCTGCT
18	P10	184 GTCCCaACTACGgCAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
19	S9	184 GTCCCcACcACGaCAATACGACGtCATGTCGATTGCTCGTTGGGGCGGCTGtTTTCTGCT
9-25	consensus	gTCCcCACTAcGaCaATACGACgcCAcGTCGAtTTGCTCGTTGGGGCGGCTgctTTCTGcT

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	245 CCGCTATGTAcGTGGGgGACCTCTGCGGATCcGTTTTCTCGTCTCTCAGCTGTTACCTT
24	T10	245 CCGCTATGTAtGTGGGaGACCTCTGCGGATCTGTTTTCTCGTCTCTCAGCTGTTACCTT
10	D3	245 CCGCCATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
9	D1	245 CCGCCATGTACGTGGGGGATCTcTGCGGATCTGTTTTCTCaTCTCCCAGCTGTTACCCcT
14	HK5	245 CCGCTATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
15	HK8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
12	HK3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCTtGTCTCCCAGCTGTTACCTT
23	T3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTCACTTT
22	SW2	245 CCGtTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTCACTTT
17	IND8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCTtGTCTCCCAGCTGTTACCTT
16	IND5	245 CCGCTATGTACGTGGGGGATCTaTGCGGATCTGTTTTCTCTcGTCTCCCAGCTGTTACCTT
21	SA10	245 CCGCcATGTACGTGGGGGAcCTCTGCGGATCTGTTTTCTTGCTCTCCCAGCTGTTACCTT
20	S45	245 CCGCTATGTACGTGGGGGAtCTCTGCGGATCTGTTTTCTTGTTtTCCCAGCTGTTACCTT
25	US6	245 CCGCTATGTACGTGGGGGAcCTCTGCGGgTCcGTTTTCTCaTCTCCCAGCTGTTACCTT
13	HK4	245 CCGCcATGTACGTGGGaGATCTCTGCGGATCTGTcTTCTCGTCTCCCAGtTGTTACCTT
18	P10	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTcTCCTCGTCTCCCAGCTGTTACCTT
19	S9	245 CCGCTATGTACGTGGGGGAcCTgTGCGGATCTGTTtTCCTCaTCTCCCAGCTGTTACCaT
9-25	consensus	CCGctATGTAcGTGGGgGAtCTcTGCGGaTCTGTtTCCTcgTcTCcCAGcTGTTACctT

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	306 tTCaCCTCGCCGGCATGAGACagcaCAGGACTGCAACTGCTCAATCTATCCCGGCCAcgTt
24	T10	306 CTCGCCTCGCCGGCATGAGACttTgCAGGACTGCAACTGCTCAATCTATCCCGGCCAtcTG
10	D3	306 CTCGCCTCGCCGGCATGAGACaGTACAGGAaTGTAAGTCTCAATCTATCCCGGCCACGTG
9	D1	306 CTCGCCTCGCCGGCATGAGACGGTACAGGAgtGTAAtTGCTCAATCTATCCCGGCCACGTG
14	HK5	306 CTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
15	HK8	306 tTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
12	HK3	306 CTCGCCTCGCCGACACGAGACAGTACAGGACTGCAACTGCTCAcTCTATCCCGGCCACGTA
23	T3	306 CTCGCCTCGCCGGCAtGAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
22	SW2	306 tTCACCTCGCCGGCacGAGACAGTACAGGACTGCAACTGtTCCATCTATCCCGGCCACGTA
17	IND8	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
16	IND5	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
21	SA10	306 CTCGCCTCGCCGGtATGAGACAGTACAGGACTGCAATTGCTCAATCTATCCCGGCCgCGTA
20	S45	306 CTCGCCTCGTCGGCATGAGACAGTACAGGACTGCAAcTGTTCAATCTATCCCGGCCACGTA
25	US6	306 CTCGCCTCGTCaGCATGAGACAGTACAGGACTGCAATTGTTCAATCTATCCCGGCCACGTA
13	HK4	306 CTCGCCTCGCCGGCATGAGACgGTACAGGACTGCAATTGcTCAATCTATCCCGGCCACGTA
18	P10	306 CTCaCCTCGCCGGCATtgGACAGTACAGGACTGCAATTGtTCAATCTATCCtGGCCACGTA
19	S9	306 CTCgCCcCGtCGGCATgaGACAGTACAGaACTGCAATTGcTCAATCTATCCcGGaCACGTg
9-25	consensus	cTCgCCtCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTCaaTCTATCCcGGcCacgTa

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FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCaCCTACAACAGCcCTAGTGc
24	T10	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCGCCTACAACAGCtCTAGTGG
10	D3	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCTACAgCAGCCCTAGTGG
9	D1	367 ACAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCtTAGTGG
14	HK5	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCCTAGTGG
15	HK8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCcACAACAGCCCTAGTGG
12	HK3	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCcCCTACAgCAGCCCTAGTGG
23	T3	367 aCAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCgCCcACAaCgGCaCTAGTGG
22	SW2	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCACCTACAGCaGCCCTgGTGG
17	IND8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCgGCCCTAGTGG
16	IND5	367 TCAGGTCACCGCATGGCcTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
21	SA10	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAaCAGCtCTAGTaG
20	S45	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCTACAGCAGCCtTAGTGG
25	US6	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAAtTGGTCACCTACAGCAGCCCTAGTGG
13	HK4	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
18	P10	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCcACAGCAGCCCTAGTGG
19	S9	367 aCAGGTCAtCGCATGGCcTGGGATATGATGATGAACTGGTCGCCtACAaCAGCCCTAGTGG
9-25	consensus	tCAGGTCaCCGcATGGCtTGGGATATGATGATGAACtGGTCaCCtACAgCaGCccTaGTgg

09084591.052699

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	428 TaTCGCAGTTACTCCGaATCCCACAAGCTGTCgTGGACATGGTGgCgGGGGCCCCACTGGGG
24	T10	428 TgTCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGaCaGGGGCCCCACTGGGG
10	D3	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCgTGGACATGGTGgCGGGGGCCCCACTGGGG
9	D1	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGgCGGGGGCCCCACTGGGG
14	HK5	428 TGTCGCAGTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTaGCGGGGGCCCCACTGGGG
15	HK8	428 TGTCGCAGTTACTCCGGATCCCGCAAGCTaTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
12	HK3	428 TGTCGCAaTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
23	T3	428 TGTCGCAGTTgCTCCGGATCCCACAAGCTGTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
22	SW2	428 TATCGCAGTTaCTCCGGATCCCACAAGCTGTCGTGGACATGGTaGCGGGGGCCCCACTGGGG
17	IND8	428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGATATGGTGgCGGGGGCCCCACTGGGG
16	IND5	428 TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGATATGGTGgCGGGGGCCCCACTGGGG
21	SA10	428 TATCGCAGTTACTCCGGATCCCACAAGCTaTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
20	S45	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCGTGGACATGGTGgCGGGGGCCCCACTGGGG
25	US6	428 TATCGCAGTTACTCCGGATCCCACAAGCTGTCATGGACATGGTGgCGGGGGCCCCACTGGGG
13	HK4	428 TATCGCAGTTACTCCGaCTCCCACAAGCTGTCATGGACATGGTGgCGGGaGCCCCACTGGGG
18	P10	428 TgTCGCAGCTACTCCGGATCCCACAAGCTaTCtTGGATgTGGTGgCGGGGGCCCCACTGGGG
19	S9	428 TaTCGCAGCTACTCCGGATCCCACAAGCTgTCaTGGATaTGGTGgCGGGGGCCCCACTGGGG
9-25	consensus	TaTCGCAGtTaCTCCGgaTCCCaCAAGCTgTCgTGGAcATGGTgCgGGgGCCCCACTGGGG

09084691.052698

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	489 AGTCCTGGCGGGCCTcGCCTACTAcTCCATGGCGGGGAAC TGGGc cAAGGTTTTAATTGTG
24	T10	489 AGTCCTGGCGGGCCTtGCCTACTATTCCATGGCGGGGAAC TGGGCTAAGGTTTTAATTGTG
10	D3	489 GGTCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
9	D1	489 GGTCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
14	HK5	489 GGTCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
15	HK8	489 AGTCCTAGCGGGCCTTGCTACTATTCCATGGTGGGcAAC TGGGCTAAGGTTTTGATTGTG
12	HK3	489 AGTCCTAGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
23	T3	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
22	SW2	489 AGTCCTGGCGGGCCTTGCaTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTG
17	IND8	489 AATCCTGGCGGGCCTTGCTACTATTCCATGGTAGGGAAC TGGGCTAAGGTTTTGATTGTG
16	IND5	489 AATCCTGGCGGGCCTTGCTACTATTCCATGGTAGGGAAC TGGGCTAAGGTTTTGATTGTG
21	SA10	489 AGTCCTaGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTTTGATTGTt
20	S45	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTCTGATTGTG
25	US6	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTTCTGATTGTG
13	HK4	489 AGTCCTaGCGGGCCTTGctTACTATTCCATGGTGGGGAAC TGGGc cAAGGTTTTGATTGTG
18	P10	489 AGTCCTGGCGGGCCTTGCTACTATTCCATGGTGGGGAAC TGGGCTAAGGtTTGATTGTG
19	S9	489 AGTCCTGGCGGGCCTcGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGtTTGATTGTG
9-25	consensus	agTCCTgGCGGGCCTtGCcTACTAtTCCATGGtgGGgAAC TGGGctAAGGttTgATTGTg

09084691.052698

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	550 tTGCTACTCTTTGCCGGCGTTGATGGG
24	T10	550 ATGCTACTCTTTGCCGGCGTTGATGGG
10	D3	550 ATGCTACTCTTTGCTGGCGTcGACGGC
9	D1	550 ATGCTACTCTTTGCTGGCGTTGACGGC
14	HK5	550 ATGCTACTtTTTGCCGGCGTTGATGGG
15	HK8	550 ATGCTACTgTTTGCCGGCGTTGATGGG
12	HK3	550 ATGCTACTtTTTGCCGGCGTTGATGGG
23	T3	550 cTGCTACTCTTTGCCGGCGTTGATGGG
22	SW2	550 ATGCTACTCTTTGCTGGCGTTGACGGG
17	IND8	550 ATGCTACTCTTTGCCGGCGTTGACGGG
16	IND5	550 ATGCTACTCTTTGCCGGCGTTGACGGG
21	SA10	550 ATGCTACTCTTTGCCGGCGTTGACGGG
20	S45	550 ATGCTACTCTTTGCCGGCGTTGACGGG
25	US6	550 tTGCTACTCTTTGCCGGCGTTGACGGG
13	HK4	550 ATGCTACTCTTTGCCGGCGTTGACGGG
18	P10	550 ATGCTACTCTTTGCCGGCGTTGACGGa
19	S9	550 ATGCTACTtTTTGCTGGtGTTGACGGg
9-25	consensus	aTGCTACTcTTTGCCcGGcGTtGAcGGg

09084691.052698

FIGURE 1C

SEQ ID NO: Isolate
 26 T2
 27 T4
 28 T9
 29 US10
 26-29 consensus

1 GCcCAAGTGAGGAACACCagccgCgGtTACATGGTGACTAACGACTGTTCCaATGAgAGC
 1 GCaCAAGTGAAGAACACCacTaaCAGCTACATGGTGACCaaACGACTGTTctAATGACAGCA
 1 GCCgAAGTGAAGAACACCAGTACCAGCTACATGGTGACaAATGACTGTTCCAACGACAGCA
 1 GtCcAAGTGAAaAACACCAGTACCAGCTatATGGTGACCaaATGACTGcTCCAACGACAGCA
 GcccAAGTGAagAACACCAGtacCaGcTAcATGGTGACCaa-GACTGtTCcAA-GAcAGCA

SEQ ID NO: Isolate
 26 T2
 27 T4
 28 T9
 29 US10
 26-29 consensus

62 TCACcTGGCAGCTCCaAGCCGCGGTtCTCCACGTCCCCGGGTGTaTCCCGTGtGAGAggct
 62 TCACtTGGCAGCTCCAGGCCGCGGTCTCCACGTCCCCGGGTGTGTCCCGTGCGAGAAaAc
 62 TCACcTGGCAACTCCAGGCCGCGGTCTCCACGTCCCCGGGTGcGTCCCGTGCGAGAgAGT
 62 TCACtTGGCAACTtgAGGctGCGGTCTCCACGTtCCCCGGGTGtGTCCCGTGCGAGAAAGT
 TCAC-TGGCA-CTccAgGCcGCGGTcCTCCACGTcCCCCGGGTGtgTCCCGTGcGAGA-agt

SEQ ID NO: Isolate
 26 T2
 27 T4
 28 T9
 29 US10
 26-29 consensus

123 GGGAAATACATCcCGaTGCTGGATACCGGTcaCACCAAACGTGGCCGTGCGGCAGCCCGGC
 123 GGGAAATACATCtCGGTGCTGGATACCGGTtTCACCAAACGTGGCCGTGCGGCAGCCCGGC
 123 tGGAAAcgCgTCgCGGTGCTGGATACCGGTCTCgCCAAACGTaGctGTGCAGCGGCCTGGC
 123 gGGAAAtaCaTCtCGGTGCTGGATACCGGTCTCaCCAAAtGTgGCcGTGCAGCGGCCTGGC
 gGGAAAtaCaTCtCGgTGCTGGATACCGGTctCaCCAAAcGTgGCcGTGC-GC-GCC-GGC

SEQ ID NO: Isolate
 26 T2
 27 T4
 28 T9
 29 US10
 26-29 consensus

184 GCtCTtACGCAGGGCTTGCGGACGCACATcGACATGGTTGTGATGTCCGCCACGCTCTGCT
 184 GCCCTCACGCAGGGCTTGCGGACGCACATtGACATGGTTGTGATGTCCGCCACGCTCTGCT
 184 GCCCTCACGCAGGGCTTGCGGACGCACATCGACATGGTTGTGATGTCCGCCACGCTCTGCT
 184 GCCCTCACGCAGGGCTTGCGGACtCACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT
 GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT

SEQ ID NO: Isolate
 26 T2
 27 T4
 28 T9
 29 US10
 26-29 consensus

245 CTGCcCTcTACGTGGGGGACCTCTGCGGCGGGGTGATGCTCGCAGCCCAGATGTTcATtGT
 245 CTGCTCTtTACGTGGGGGACCTCTGCGGCGGGGTGATGCTCGCAGCCCAGATGTTcATcGT
 245 CCGCTCTcTACGTGGGGGAtCTCTGCGGCGGGGTaATGCTCGCcGCtCAGATGTTcATTaT
 245 CCGCTCTtTACGTGGGGGActTCTGCGGtGGGaTgATGCTCGCaGCCcAaATGTTcATTgT
 C-GCtCT-TACGTGGGGGAccTCTGCGGcGGGgTgATGCTCGCaGCCcAgATGTTcATTgT

[illegible]

SEQ ID NO:	Isolate	
26	T2	367 ACTGGACACCGTATGGCATGGGAcATGATGATGAACTGGTCGCCCACaGCCACCATGATCC
27	T4	367 ACTGGACACCGTATGGCATGGGA ^t ATGATGATGAACTGGTCGCCCACgGCCACCATGATCC
28	T9	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACTGGTCGCCCACaaCCACCATGATCt
29	US10	367 ACcGGgCACCGTATGGCATGGGACATGATGATGAACTGGTCGCCCACggCCACttTGATCc
26-29	consensus	ACtGGaCACCGTATGGCATGGGAcATGATGATGAACTGGTCGCCCAC-gCCACcaTGATCc

[illegible]

84892_1

FIGURE 1D

SEQ ID NO: Isolate

33 T8

30 DK8

32 SW3

31 DK11

30-33 consensus

1 GTGGAAGTtAGaAACAcCAGTTtTAGCTACTACGCCACCAATGATTGCTCgAACAAACAGCA
 1 GTGGAAGTCAGGAACATCAGTTTCAGCTACTACGCCACCAATGATTGCTCAAACAACAGCA
 1 GTGGAAGTCAGGAACATCAGTTCTAGCTACTAtGCCACCAATGATTGCTCAAACAgCAGCA
 1 GTGGAAGTCAGGAACAcCAGTTCTAGtTACTAcGCCACCAATGATTGCTCAAACAaCAGCA
 GTGGAAGTcAGgAACa - CAGTTtTAGcTACTAcGCCACCAATGATTGCTCaAACAAcCAGCA

SEQ ID NO: Isolate

33 T8

30 DK8

32 SW3

31 DK11

30-33 consensus

62 TCACCTGGCAgCTCACCaaCGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
 62 TCACCTGGCAACTCACCgACGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
 62 TCACCTGGCAACTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCCgTGTGAGAATGA
 62 TCACCTGGCAACTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA
 TCACCTGGCAaCTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA

SEQ ID NO: Isolate

33 T8

30 DK8

32 SW3

31 DK11

30-33 consensus

123 CAATGGCACCTtTGCGCTGCTGGATACAAGTaACACCTAATGTGGCTGTGAAACACCGtGGC
 123 CAATGGCACCTTGCGCTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC
 123 tAATGGCACCTTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC
 123 cAATGGCACCTTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC
 cAATGGCACCTtTGC - CTGCTGGATACAAGTgACACCTAATGTGGCTGTGAAACACCGcGGC

SEQ ID NO: Isolate

33 T8

30 DK8

32 SW3

31 DK11

30-33 consensus

184 GCACTcACTCaaACCTGCGAACgCatGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
 184 GCACTtACTCatAACCTGCGAACACACGTGCGACGTGATCGTAATGGCAGCTACGGTCTGCT
 184 GCgCTCACTCACAACCTGCGAGCACACGTGATATGATCGTAATGGCAGCTACGGTCTGCT
 184 GCaCTCACTCACAACCTGCGAGCACAtaTaGATATGATtGTAATGGCAGCTACGGTCTGCT
 GCaCTcACTCaaACCTGCGA - CaCA - gTcGA - - TGATcGTAATGGCAGCTACGGTCTGCT

SEQ ID NO: Isolate

33 T8

30 DK8

32 SW3

31 DK11

30-33 consensus

245 CGGCCTTGATGTGGGgGACGTgTGCGGGGCCGTGATGATaGcGTCGAGGCTtTCATAAT
 245 CGGCCTTGATGTGGGAGACGtATGCGGGGCCGTGATGATCGTGTCGAGGCTtTCATAAT
 245 CGGCCTTGATGTGGGAGACaTGTCGGGGCCGTGATGATCGTGTCGAGGCTTTTCATAAT
 245 CGGCCTTGATGTGGGAGACgTGTCGGGGCCGTGATGATCGTGTCGAGGCTTTTCATAgT
 CGGCCTTGATGTGGGaGACgTgTGCGGGGCCGTGATGATcGtGTCGAGGCTtTCATAaT

[illegible]

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090671-090699

1 tTAGAGTGGCGGAATGTGTCcGGCCTCTAcGTCCTTACCAACGACTGTtCCAATAGCAGTA
1 CTAGAGTGGCGGAATGTGTCCTGGCCTCTATGTCCTTACCAACGACTGTcCCAATAGCAGTA
1 CTAGAGTGGCGGAATACGTCCTGGCCTCTATGTCCTcACCAACGACTGTTCCAATAGCAGTA
1 CTAGAGTGGCGGAATACGTCCTGGCCTCTATaTCCTTACCAACGACTGTTCCAATAGCAGTA
1 CTAGAGTGGCGGAATACGTCCTGGCCTCTATgTCCTTACCAACGACTGTTCCAATAGCAGTA
cTAGAGTGGCGGAATacGTCTcGGCCTCTAtgTCCTtACCAACGACTGTtCCAATAGCAGTA

62 TcGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTT CAGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTT CAGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTT CAGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTT CAGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCCGGCTGTGTACCTTGTGTT CAGGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

TtGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTT CAGGA

123 CCGCAATACATCCACGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTCGGA
 |||||
 123 CCGCAATACATCCACGTGCTGGACCTCgGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
 |||||
 123 CCGtAATACATCCACGTGCTGGACCCcAGTGACACCTACAGTGGCAGTCAGGTAtGTCGGA
 |||||
 123 CCGCAATACATCCACGTGCTGGACCCcAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA
 |||||
 123 CCGCAATACATCCAtGTGCTGGACCCcAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA
 |||||
 CCGcAATACATCCaAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGGTAcGTCGGA

184 GCAACCACCGCtTCGATACGCAGTCATGTGGACCTGcTAGTGGGCGCGGCCACGATGTGCT
| | | | |
184 GCAACCACCGCcTCGATACGCAGTCATGTGGACCTGTTAGTGGGCGCGGCCACGATGTGCT
| | | | |
184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTgGTGGGCGCGGCCAcATGTGCT
| | | | |
184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT
| | | | |
184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT
| | | | |
GCAACCACCGCtTCGATACGCAGTCATGTGGACCTatTaGTGGGCGCGGCCACgaTGTGCT

FIGURE 1E

SEQ ID NO: Isolate

35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

245 CTGCGCTCTACGTGGGtGATgTGTGTGGGGCCGTCTTCCTtGTGGGACAAGCCTTCACGTT
 245 CTGCGCTCTACGTGGGcGATATGTGTGGGGCCGTCTTCCTCGTGGGACAAGCCTTCACGTT
 245 CTGCGCTCTACGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
 245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
 245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
 CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT

SEQ ID NO: Isolate

35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

306 CAGACcTCGTGCGCCATCAAACaGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAtCTT
 306 CAGACCgCGTCGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAcCTT
 306 CAGACCTCGTCGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATCTT
 306 CAGACCTCGTCGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATCTT
 306 CAGACCTCGTCGCGCCATCAAACGGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCATgTT
 CAGACcTCGTGCGCCATCAAACgGTCCAGACCTGTAACtGCTCGCTGTACCCAGGCCAtcTT

SEQ ID NO: Isolate

35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGctGTGGGTATGGTGG
 367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCcGTGGGTATGGTGG
 367 TCAGGACATCGcATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
 367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
 367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGctGTGGGTATGGTGG

SEQ ID NO: Isolate

35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

428 TaGCGCACGTCTGCGtCTGCCCCAGACCTTGTTTCGACATAATAGctGGGGCCCATTTGGGG
 428 TGGCGCACGTCTGCGgTTGCCCCAGACCTTGTTTCGACATAATAGCCGGGGCCCATTTGGGG
 428 TGGCGCACGTtCTGCGtTTGCCCCAGACCgTGTTTCGACATAATAGCCGGGGCCCATTTGGGG
 428 TGGCGCACATCCTGCGATTGCCCCAGACCTTGTTTTCGACATACTGGCCGGGGCCCATTTGGGG
 428 TGGCGCACATCCTGCGATTGCCCCAGACCTTGTTTTCGACATACTGGCCGGGGCCCATTTGGGG
 TgGCGCACgTcCTGCG - tTGCCCCAGACCTTGTTTCGACATAaTaGcCGGGGCCCATTTGGGG

FIGURE 1E

SEQ ID NO: Isolate

35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

489 CATCaTGGCgGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
 |||
 489 CATCTTGGCaGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
 |||
 489 CATCTTGGCGGGCCTAGCCTATTACTCCATGCAaGGCAACTGGGCCAAGGTCGCTATCATC
 |||
 489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
 |||
 489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATtgTC
 |||
 CATCtTGGCgGGCCTAGCCTATTAcTCcATGCagGGCAACTGGGCCAAGGTCGCTATcaTC

SEQ ID NO: Isolate

35 DK12

36 HK10

37 S2

39 S54

38 S52

35-39 consensus

550 ATGGTTATGTTTTTCAGGaGTCGATGCC
 |||
 550 ATGGTTATGTTTTTCAGGGGTCGATGCC
 |||
 550 ATGGTTATGTTTTTCAGGGGTCGAcGCC
 |||
 550 ATGATTATGTTTTTCAGGGGTCGATGCC
 |||
 550 ATGATTATGTTTTTCAGGGGTCGATGCC
 |||
 ATGgTTATGTTTTTCAGGgGTCGAtGCC

00004591.052593

Subpopulation		Age		Sex		Marital Status		Education		Occupation		Income		Health Status		Social Support		Life Satisfaction	
Group	Sample Size	Mean	SD	Male	Female	Married	Single	High	Low	Professional	Unemployed	High	Low	Good	Poor	High	Low	High	Low
1	100	45.2	12.5	55	45	60	40	70	30	60	40	50	50	70	30	60	40	70	30
2	100	48.5	11.8	52	48	58	42	65	35	55	45	45	55	65	35	55	45	65	35
3	100	51.0	13.2	50	50	55	45	60	40	50	50	40	60	50	50	50	50	50	50
4	100	54.5	14.0	48	52	50	50	55	45	45	55	35	65	40	60	40	60	40	60
5	100	58.0	15.5	45	55	45	55	50	50	40	60	30	70	30	70	30	70	30	70
6	100	61.5	16.0	42	58	40	60	45	55	35	65	25	75	25	75	25	75	25	75
7	100	65.0	17.0	40	60	35	65	40	60	30	70	20	80	20	80	20	80	20	80
8	100	68.5	18.0	38	62	30	70	35	65	25	75	15	85	15	85	15	85	15	85
9	100	72.0	19.0	35	65	25	75	30	70	20	80	10	90	10	90	10	90	10	90
10	100	75.5	20.0	32	68	20	80	25	75	15	85	5	95	5	95	5	95	5	95

43 27

42 26

1 GTcAACTATCaCAATGCCTCGGGCGTCTATCACATCACCAACGACTGCCGAACTCGAGCA
1 GTtAACTATCGCAATGCCTCGGGCGTCTATCACGTACCAACGACTGCCGAACTCGAGCA
GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCGAACTCGAGCA

43 27

42 26

62 TAA TGTATGAGGCCGAACACCACATCCTACACCTCCCAGGGGTGCGTACCCTGTGTGAGGGa
62 TAGTGTATGAGGCCGAACACCAgATCTTACACCTCCCAGGGGTGcTgCCCTGTGTGAGGGt
TagTGTATGAGGCCGAACACCAgATCtTACACCTCCCAGGGGTGcTgCCCTGTGTGAGGGt

43 27

42 26

123 gGGGAACCAAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGcGcCTTATATCGGT
123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT
tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT

43 27

42 26

184 GCaCCGCTTGAaTCCaTCCGGAGACATGTGGACCTGATGGTAGGCGCtGCTACaGTGTGCT
 184 GCTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTGGGCGCCGCTACTGTaTGCT
 GcTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTgGGCGCcGCTACtGTaTGCT

13 27

12 26

245 CcGcTcCTCTACaTTGGGGACCTGTGCGGTGGcGtATTtTTGGTTGGtCAGATGTTtTCCTTT
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
245 CtGCCCTCTACgTTGGAGAtCTGTGCGGTGGTGcATTCTTGGTTGGcCAGATGTTCTCCTT

CtGCCCTCTACgTTGGaGAtCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTtTCcTT

13 **27**

26

306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTATGCgGGGCacgTt
 306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCTATCTACGCAGGGCATATC
 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCTATCTACGCaGGGCataTc

3 27

2 26

367 ACaGGCCACAGaATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCTtTGgTCC
 367 ACgGGCCACAGgATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCTGcTtC
 ACgGGCCACAGgATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCTgTgTtC

FIGURE 1F

SEQ ID NO: Isolate
 43 Z7
 42 Z6
 42-43 consensus (Z6)

428 TCGCCCAGGTtATGAGGATCCCTAGCACTCTGGTgGACCTACTCaCTGGAGGGCACTGGG
 |||||
 428 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCGCTGGAGGGCACTGGGC
 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTaGAtCTACTCgCTGGAGGGCACTGGGC

SEQ ID NO: Isolate
 43 Z7
 42 Z6
 42-43 consensus (Z6)

489 taTCCTTaTcGGGgTGGCaTACTTcTGCATGCAAGCTAATTGGGCCAAGGTCATtCTGGTC
 |||||
 489 CgTCCTTGTTGGGtTGGCGTACTTCAGtATGCAAGCTAATTGGGCCAAaGTCATCCTGGTC
 cgTCCTTgTtGGGtTGGCgTACTTCaGtATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC

SEQ ID NO: Isolate
 43 Z7
 42 Z6
 42-43 consensus (Z6)

550 CTTTTCTCTaCGCTGGAGTTGATGCC
 |||||
 550 CTTTTCTCTtCGCTGGAGTTGATGCC
 CTTTTCTCTtCGCTGGAGTTGATGCC

09084691.052698

FIGURE 1G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	184 GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGACTACTTAGCGGGAGGaGCTGctCTCTGcT
47	SA5	184 GCGGTCACGGCTCCTCTTCGGAGGGtCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGcT
49	SA7	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACcTAGCGGGAGGGGCTGCCCTCTGcT
46	SA4	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGcT
50	SA13	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGgGGGGCTGCCCTtTGcT
48	SA6	184 GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGAtTACTTgGCGGGaGGGGCcGCCCTgTGCT
45-50	consensus	GCGGTCACGGCTCCTCTTCGGAGGGcCGTTGAcTACtTaGCGGGaGGgGcTGCcTcTGCT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	245 CCGCACTATACGTCGGcGACGCGTGCGGGGCAGTGTTtCTGGTAGGCCAAATGTTcACCTA
47	SA5	245 CCGCACTATACGTCGGGGACGCGTGCGGGGCAGTGTTcTTGGTAGGCCAAATGTTcACCTA
49	SA7	245 CCGCgCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAgATGTTcAgCTA
46	SA4	245 CCGCaCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAAATGTTcACCTA
50	SA13	245 CCGCGTTATACGTCGGAGACGCGTGCGGGGCAGTGTTTTTGGTAGGtCAAATGTTcACCTA
48	SA6	245 CCGCGTTATACGTCGGAGACGtGTGCGGGGCAtTGTTTTTGGTAGGcCAAATGTTcACCTA
45-50	consensus	CCGC - cTATACGTCGGgGACGcGTGCGGGGCAGTGTTtCTGGTAGGcCaAATGTTcAcCTA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	306 TAGGCCTCGCCAGCATAcAcAGTGcAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
47	SA5	306 TAGGCCTCGCCAGCATAcTACGGTGcAGGACTGCAACTGTTCCATTTACAGcGGCCATATC
49	SA7	306 TAGGCCTCGCCAGCACACTACGGTGcAGGACTGCAACTGTTCCATTTACAGTGGCCATATC
46	SA4	306 TAGGCCTCGCCAGCACACTACGGTGCAaGACTGCAATGcTCtATTACAGTGGCCATATC
50	SA13	306 TAGcCCTCGCCgGCATAaTgttGTGcAGGACTGCAACTGtTCCATTTACAGTGGCCAcATC
48	SA6	306 TAGgCCTCGCCaGCATgcTacgGTaCAGGACTGCAACTGcTCCATTTACAGTGGCCAtATC
45-50	consensus	TAGgCCTCGCCaGCAtactacgGTgCAGGACTGCAAcTgTTCcATTACAGtGGCCAtATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	367 ACCGGCCACCGgATGGCtTGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGcTGA
47	SA5	367 ACCGGCCACCGAATGGCATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGGTGA
49	SA7	367 ACCGGCCACCGAATGGCATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTGGTGA
46	SA4	367 ACCGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCTACGACgGCCTTGcTGA
50	SA13	367 ACCGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCTACaACAGCtTTGGTGA
48	SA6	367 ACTGGCCACCGGATGGCATGGGACATGATGATGAATTGGTCACCcgCgACAGCtTTGGTGA
45-50	consensus	ACcGGCCACCGgATGGCaTGGGACATGATGATGAATTGGTCACCTaCgACaGCcTTGgTGA

FIGURE 1G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	428 TGGCCCAGaTGCTACGGATcCCCCAgGTGGTCATaGACATCATaGCCGGGGGCCACTGGGG
47	SA5	428 TGGCCCAGgTGCTACGGATTCCCCAaGTGGTCATtGACATCATTGCCGGGGGCCACTGGGG
49	SA7	428 TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
46	SA4	428 TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
50	SA13	428 TGGCCCAGTTGtTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGcCCACTGGGG
48	SA6	428 TGGCCCAaaTGcTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGgCCACTGGGG
45-50	consensus	TGGCCCAGtTGcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	489 GGTCTTGTTtGCCGcCGCATACTTtGCGTCgGCcGCcAACTGGGCTAAGGTaGTGCTGGTt
47	SA5	489 GGTCTTGTTcGCCGtCGCATACTTCGCGTCAGCGGCTAACTGGGCTAAGGTTGTGCTGGTC
49	SA7	489 GGTCTTGTTcGCCGCCGCATATTTcGCGTCAGCGGCTAACTGGGCTAAGGTTGTGCTGGTC
46	SA4	489 GGTCTTGTTtGCCGCCGCATATTTcGCGTCAGCGGCTAACTGGGCTAAGGTTaTaCTGGTC
50	SA13	489 GGTCTTGTTcGCCGCCGCATACTaCGCGTCGGCGGCTAACTGGGcAAGGTTGTGCTGGTC
48	SA6	489 GGTCTTGTTcGCCCGcGCATACTtCGCGTCGGCGGCTAACTGGGctAAGGTTGTGCTGGTC
45-50	consensus	GGTCTTGTTcGCCGccGCATAcTtCGCGTC - GCgGcTAACTGGGctAAGGTTgTgCTGGTc

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	550 CTGTTcCTGTTTGCGGGGGTCGATGGC
47	SA5	550 CTGTTTCTGTTTGCGGGGGTCGATGGC
49	SA7	550 TTGTTTCTGTTTGCGGGGGTCGATGCC
46	SA4	550 TTGTTTCTGTTTGCGGGGGTCGATGCC
50	SA13	550 cTGTTTCTGTTTGCGGGGGTCGATGCC
48	SA6	550 tTGTTTCTGTTTGCGGGGGTtGATGCC
45-50	consensus	-TGTTtCTGTTTGCGGGGGTcGATGcC

FIGURE 1H

SEQ ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

SEQ ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

SEQ ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

1 GTGGAAGTcAGgAACAtCAGTTctAGcTACTAcGCCACCAATGATTGCTCaAACaACAGCA
 1 GTGGAGGTCAAGGACACCGGCGACTCCTACATGCCGACCAACGATTGCTCCAACCTAGTA
 1 GcccAAGTGAagAACACCAgtacCaGcTAcATGGTGACcAACGACTGtTCCaAtGAcAGCA
 1 cTAGAGTGGCGGAATacGTCTGGCCTCTAtgTCCTtACCAACGACTGtTCCAATAGCAGTA
 1 tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACgAACGACTGcTCCAACtcaAGca
 1 tACCAAGTgCGCAACTCcaCgGGgCTtTACCATGTcACCAATGAtTGCCCTAAcTCGAGtA
 1 GAGCACTACCGGAATGCTTCGGGCGATCTATCACAATGATTGTCCGAATTCCAGTA
 1 GTtAACTATCgCAATGCCTCGGGCGTCTATCACgTCACCAACGACTGCCCGAACTCGAGCA
 1 TACAACtATCGCAACAGCTCGGGTGTCTACCATGTCACCAACGATTGCCCGAACTCGAGCA
 1 GTGCACTACCGGAATGCTTCGGGCGTCTATCATGTcACCAATGATTGCCCaAACTCtTCCA
 1 GTtCCcTACCGaAAtGCCTCtGGGGTtTAtCATGTcACCAATGAtTGCCCaAACTCtTCCA
 1 CTTACCTACGGCAACTCCAGTGGGCTATACCATCTCACAATGATTGCCCAACTCCAGCA

A

TA

AC AA GA TG C AA

62 TCACCTGGCAaACTCACCaaACGCAgttCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA
 62 TCGTTTGGCAGCTTGAAGGAGCAGTGCTTCATACTCCTGGATGCGTCCCTTGTGAGCGTAC
 62 TCACcTGGCAaACTccAgGCcCGGGTcCTCCACGTcCCCGGGTgTgTCCCGTGcGAGaaagt
 62 TtGTGTATGAGGCCGATGACGTcATTCTGCACACACcTGGCTGTGTACCTTGTGTTCAGGA
 62 TtGTGTatGAggCAgcgGACaTGATcaTGCAcACcCCcGGgTGcgTgCCCTGcGtTcGgGA
 62 TtGTGTACGAGgCgGCcGATgCcAtcCTgCacaCtCCgGGgTGtGTcCCTTGCgTTCGcGA
 62 TAGTCTATGAAGCTGACCATCACATCTACACTTGCCGGGTGCGTACCCTGTGTGATGAC
 62 TAGTGTATGAGGCCGAACACCagATCtTACACCTCCCGGGTGTGCTACCCTGTGTGATGAC
 62 TAGTCTATGAAACCGATTACCACATCTTACACCTCCCGGGATGCGTTCCTTGCgTGAGGGT
 62 TAGTGTACGAGACGGAGCACCACATCATGCACTTGCCAGGGTGTGTCCCTGTGTGCGGAC
 62 TaGTcTAcGAGGCTGAtaaCCTGATctTgCAcGCACCTGGtTGCGTGCCcTGTGTcaggca
 62 TCGTGCTGGAGGCGGATGCTATGATCTTGCATTGCGCTGGATGCTTGCTTGTGTGAGGGT

T

A

T T CA

CC GG TG T CC TG G

123 cAATGGCACCCcTGCgCTGCTGGATACAAGTgACACCTAATGTGGCTGTGAAACACCGcGGC
 123 CGCCAACGTCTCTCGATGTTGGGTGCCGGTTGCCCCCAATCTCGCCATAAGTCAACCTGGC
 123 gGGAAAtaCaTcTcGgTGCTGGATACCGGTctCaCCAAAcGTgGCcGTGCaGCaGCCcGGC
 123 CGGcAATACATCcAcGTGCTGGACCCcAgTGACaCCTACaGTGGCAGTCAGGTAcGTCCGA
 123 gaacAAActcCTCccgcTGcTGGGTaGCGCTcaCtCCACgCTcGCgGCCcAGGAAcgcAgc
 123 GGgTaaCgcctCGAggTGTGGGTGgCGgTGaCCCCCACgGTgGCCACcAGGGAcGGCAaa
 123 TGGGAACACATCGCGTGTGCTGGACGCCGTGACGCCTACAGTGGCTGTGCGCACACCCGGGC
 123 tGGGAAtCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT
 123 AGGGAACAAGTCTACATGCTGGGTGTCTCTACCCCCACCGTGGCTGCGCAACATCTGAAT
 123 GGAGAATACTTCTCGTGCTGGGTGCCCTTGACCCCCACTGTGGCCGCCCTATCCCAAC
 123 agaTAATGTcAGTAggTGCTGGGTcCAaATCACCCCCACatTgTCAGCCCCGAaccTCGGA
 123 CGATGATCGGTCCACCTGTTGGCATGCTGTGACCCCCACCTGGCCATACCAATGCTTCC

TG TGG

T C CC A T C

FIGURE 1H

SEQ ID NO:	Genotype	
30-33	(IV/2b)	184 GCaCTcACTCacAACCTGCGAaCaCATgTcGacaTGATcGTAATGGCAGCTACGGTCTGCT
34	(2c)	184 GCTCTCACTAAGGGCCCTGCGAGCACACATCGATATCATCGTGATGTCTGCTACGGTCTGTT
26-29	(III/2a)	184 GCcCTcACGCAGGGCTTGGCGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
35-39	(V/3a)	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTatTaGTGGCGCGGCCACgaTGTGCT
9-25	(II/1b)	184 gTCcCcActAcGaCaATACGACgcCAcGTcGATtTTGCTCGTTGGGGCGGCTgctTTCTGcT
1-8	(I/1a)	184 CTCCCCgCAaCGCAGCTtCGACGTcACATCGATCTGCTtGTcGGgAGcGCCACCCTCTGcT
40	(4a)	184 GCTCCGCTTGAGTCGTTCCGGCGACATGTGGACTTAATGGTAGGGCGCGGCCACTTTGTGTT
42-43	(4c)	184 GCTCCGCTTGAGTCCTTGGAGACGTACGTGGATCTGATGGTGGGCGGCCACTCTCTGCT
44	(4d)	184 GCTCCGCTTGAGTCCTTGGAGACGTACGTGGATCTGATGGTGGGCGGCCACTCTCTGCT
41	(4b)	184 GCACCGTTAGAGTCCATGCGCAGGCATGTAGACCTGATGGTGGGTGCGGCTACTATGTGTT
45-50	(5a)	184 GCGGTACGGCTCCTCTTCGGAGGGcCGTTGAcTAcTaGCGGGaGGgGCTGcCCTcTGCT
51	(6a)	184 ACGCCCGCAACGGGATTCCGCAGGCATGTGGATCTTCTTGGGGCGCCGAGTGGTTTGCT
1-51	consensus	T G T GA T G GC T TG T
SEQ ID NO:	Genotype	
30-33	(IV/2b)	245 CGGCCTTGATGTGGGaGACgTgTGCGGGGGCCGTGATGATcGtGTCGCAGGCTtTCATAaT
34	(2c)	245 CTGCCCTTTATGTGGGGGACGTGTGTGGCGCGCTGATGCTGGCCGCTCAGGTCTGCTCGT
26-29	(III/2a)	245 CcGCTcTtTACGTGGGGGAaccTCTGCGGcGGGgTgATGCTCGCaGcCaGATGTTcATtGt
35-39	(V/3a)	245 CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT
9-25	(II/1b)	245 CCGctATGTAcGTGGGgGATCTcTGCGGaTCTGtTtTCCTcGTcTcCAGcTGTTCACctT
1-8	(I/1a)	245 CGGCCCTCTAcGTGGGGGACTGTGCGGGTCTGTCTTtCTtGTcGtCaACTGTTcACctT
40	(4a)	245 CTGCCCTCTATGTTGGGGACCTCTGCGAGGTGCCTTCTGATGGGGCAGATGATCACTTT
42-43	(4c)	245 CtGCCCTCTACgTTGGaGATCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCcTT
44	(4d)	245 CCGCCCTCTACATCGGAGACGTGTGTGGGGTGTGTTCTTGGTGGTCAACTGTTcACCTT
41	(4b)	245 CCGCCTTCTACATTGGAGATCTGTGTGGAGGCGTCTTCTAGTGGGGCAGCTGTTTCGACTT
45-50	(5a)	245 CCGCgCTATACGTCCGGgGACGcGTGCGGGGcAgTGTtTtTGGTAGGcCaATGTTcAcCTA
51	(6a)	245 CATCCCTGTACATCGGGGACCTGTGTGGCTCTCTTTTTGGCGGGACAACCTATTACCTT
1-51	consensus	C T TA T GG GA TG GG T T CA T
SEQ ID NO:	Genotype	
30-33	(IV/2b)	306 ATCGCCaGAACgCCACaACTTtACCCaAGAGTGCAACTGTTCCATCTACCAAGGTCatATC
34	(2c)	306 GTCGCCACAACACCATAACGTTTGTCCAGGAATGCAACTGTTCCATATACCCGGGCGCATT
26-29	(III/2a)	306 CTCGCCGCaACacCACTgGTTTGTGCaAGaTGCAATTGCTCcAtcTACCctGGtACCATC
35-39	(V/3a)	306 CAGACCTcGTTCGCCATCAAAcGgTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAtcTT
9-25	(II/1b)	306 cTCgCCTcGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTcaTCTATCCcGGcCacgTa
1-8	(I/1a)	306 cTCTCCcAGgCgCCaCTGGACaACGCaAGaCTGcAAcTGcTcaTCTATCCcGGcCacgTa
40	(4a)	306 TCGGCCCGCTCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC
42-43	(4c)	306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCTcATCTAcGCaGGGCataTc
44	(4d)	306 CCAACCTCGCCGCCACTGGACCACCCAGGACTGCAATTGTTCCATCTACACAGGACATATC
41	(4b)	306 CCGACCGCGCCGGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC
45-50	(5a)	306 TAGgCCTCGCCaGCaTactacgTgCAGGACTGCAAcTGTtTcATTtACAGtGGCCatATC
51	(6a)	306 TCAGCCCCCGCGTCATTGGACTGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC
1-51	consensus	CC C CA TG AA TG TC T TA GG T
SEQ ID NO:	Genotype	
30-33	(IV/2b)	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCTtACCATGATCC
34	(2c)	367 ACGGGACACCGCATGGCTTGGGATATGATGATGAACCTGGTCGCCCCACTACCACCATGCTCC
26-29	(III/2a)	367 ActGGaCACCgTATGGCATGGGAcATGATGATGAACCTGGTCGCCCCACgCCACcaTGATCc
35-39	(V/3a)	367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
9-25	(II/1b)	367 tCAGGTCAcCGcATGGCtTGGGAtATGATGATGAACCTGGTCaCCTACAgCaGCcTaGTgg
1-8	(I/1a)	367 ACGGGtCAcCGcATGGCaTGGGATATGATGATGAACCTGGTCCCCtACGaCgGCcTGGTg
40	(4a)	367 ACCGGCCACAGGATGGCGTGGGACATGATGATGAACCTGGAGCCCTACCACCACTCTGCTCC
42-43	(4c)	367 ACgGGCCACAGgATGGCATGGGACATGATGATGAACCTGGAGTCCCAcACCACCTGcTtC
44	(4d)	367 ACAGGACACAGAATGGCTTGGGACATGATGATGAACCTGGAGCCCTACCAGCGCGCTGATTA
41	(4b)	367 TCGGGCCACAGGATGGCTTGGGACATGATGATGAACCTGGAGCCCTACCAGCGCGCTGATTA
45-50	(5a)	367 ACcGGCCACCGgATGGCaTGGGACATGATGATGAATTGGTCACCTaCgACaGcCTTgTGA
51	(6a)	367 ACCGGCCACAGGATGGCTTGGGACATGATGATGAACCTGGTCACCCACAACCACTCTGGTCC
1-51	consensus	C GG CA G ATGGC TGGGA ATGATG T AA TGG CC C T T

FIGURE 1H

SEQ ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

428 TcGCCTAtGCcGcTcGTGTtCCTGAgCTAGtCCTtgAaGTtGTCTTCGGcGGcCATTGGGG
 428 TGGCGTACTTGGTGCGCATCCCCGGAAGTCATCTTGGATATTGTTACAGGAGGTCAATTGGGG
 428 TGGCGTACGcGATGCGCGTTCCTCGAGGTCACTaTAGACATCaTtaGCGGgGcTCACTGGGG
 428 TgGCGCACgTcCTGCGtTtGCCCCAGACcTGTTCGACATAaTaGcCGGGGCCCACTGGGG
 428 TaTCGCAgtTaCTCCGgaTCCCaCAAGCTgTCgTGGAcATGGTggGgGGgCCCCACTGGGG
 428 TaGcTcAGCTGCTCcGGaTCCCGCaAGCCaTCTTGGAcATGATCGCTGGTGCcCACTGGGG
 428 TCGCCCAGATCATGAGGGTCCCCACAGCCTTCTCGACATGGTTGCCGGAGGCCACTGGGG
 428 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTAgAtCTACTCgCTGGAGGGCACTGGGG
 428 TCGCCCAACTTATGAGGATCCCAGGCGCCATGGTCGACCTGCTTGCAGGCGGCCACTGGGG
 428 TGGCTCAGATCTTACGGATCCCCCTCTATCCTAGGTGACTTGCTCACCGGGGGTCACTGGGG
 428 TGGCCCAgtTGcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG
 428 TATCTAGCATCTTGAGGGTACCTGAGATTTGTGCGAGTGTGATATTTGGTGGCCATTGGGG

T C

G T CC

T T GG G CA TGGG

SEQ ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

489 cGTGGTGTtTGGCTTGGCCTATTTCTCCATGCagGGAGCGTGGGCCAAaGTCATtGCCATC
 489 TGTAATGTtTGGCCTCGCTTACTTCTCCATGCAGGGATCGTGGGCGAAGGTCATCGTTATC
 489 CGTCaTGTTcGGCtTaGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAaGTCgTTGTATC
 489 CATCtTGGCgGGCCTAGCCTATTaTcCaATGCagGGCAACTGGGCCAAGGTGCTATcaTC
 489 agTCCTgGCGGGCCTtGCcTACTAtTCCATGGtggGgAACTGGGCTaAGGTtTgATTGTg
 489 AGTCCTaGCGGGCATAGCGTATTTcTCCATGGtGGGgAACTGGGCGAAGGTCCtTgTAgTg
 489 CGTCCTCGCGGGCTTGGCGTACTTcAGCATGCAAGGCAATTGGGCCAAGGTAGTCCTGGTC
 489 cgTCCTTgTtGGGtTGGCgTACTTcAgTATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC
 489 CATTCTGGTTGGCATAGCGTACTTcAGCATGCAAGCTAATTGGGCCAAGGTATCCTGGTC
 489 AGTTCTTGCTGGTCTAGCTTTCTTcAGCATGCAGAGTAaCTGGGCGAAGGTATCCTGGTC
 489 GGTCTTGTTcGCCGcGCATAcTtCGCGTCgGCgGCTaACTGGGCTaAGGTtTgTgCTGGTc
 489 GATACTACTAGCCGTTGCCTACTTTGGCATGGCTGGCAACTGGCTAAAAGTTCTGGCTGTT

T T G GC T T

TGG AA GT

T

SEQ ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

550 CTCCTtCTTGTcGCAGGAGTGGAtGCA
 550 CTCCTGCTGACTGTCTGGGGTGGAGGCG
 550 CTtTGCTggCcGCTGGgGTGGACGCG
 550 ATGgTTATGTTTTTCAGGgGTcGAtGCC
 550 aTGCTACTcTTTGCcGGcGTtGAcGGg
 550 CTGtTGCTgTtTgCCGGCGTcGAtGCG
 550 CTTTTCTCTTTGCTGGGGTAGACGCC
 550 CTTTTCTCTcCGCTGGAGTTGATGCC
 550 CTGTTTCTCTTTGCTGGAGTCGACGCT
 550 CTATTCTCTTTGCCGGGGTTCGAGGGA
 550 tTGTTtCTGTTTGCGGGGTcGATGcC
 550 CTGTTCTATTTCAGGGGTGAAGCA

T T T C GG GT GA G

FIGURE 2A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	1 YQVRNSTGLYHVTNDCPNSSIVYEtADAILHaPGCVPCVREGNtSRCWVAMTPTVATRDGK
52	DK7	1 YQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNvSRCWVAMTPTVATRDGK
59	US11	1 YQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNaSRCWVAMTPTVATRDGK
55	DR4	1 HQVRNSTGLYHVTNDCPNSSIVYEADAILHTPGCVPCVREGNtSRCWVAVTPTVATRDGK
54	DR1	1 HQVRNSTGLYHVTNDCPNSSIVYEADAILHaPGCVPCVREGNaSRCWVAVTPTVATRDGK
53	DK9	1 YQVRNSSGLYHVTNDCPNSSIVYEADAILHSPGCVPCVREGNASKCWVAVAPTPTVATRDGK
58	SW1	1 YQVRNSSGLYHVTNDCPNSSIVYETADAILHSPGCVPCVREdGApKCWVAVAPTPTVATRDGK
57	S18	1 YQVRNSTGLYHVTNDCPNSSIVYETADtILHSPGCVPCVREGnAsrCWVpVAPTPTVATRDGK
52-59	consensus	yQVRNSTGLYHVTNDCPNSSIVYEaADaILH - PGCVP CVREgnasrCWVavtPTVATRDGK

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	62 LPatQLRRyIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRlWTTQdCNCsIYPGHI
52	DK7	62 LPTaQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQGCNCsIYPGHI
59	US11	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQGCNCsIYPGHI
55	DR4	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRhWTTQdCNCsIYPGHI
54	DR1	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQdCNCsIYPGHI
53	DK9	62 LPATQLRRHIDLLVGSATLCSALYVGDLGGSVFLVGQLFTFSPrRHWTtQdCNCsIYPGHI
58	SW1	62 LPATQLRRHIDLLVGSATLCSALYVGDLGGSVFLVSQLFTFSPrRHWTtQdCNCsIYPGHI
57	S18	62 LPATQLRRHIDLLVGSATLCSALYVGDLGGSVFLVSQLFTiSPRRHWTtQdCNCsIYPGHI
52-59	consensus	LP-tQLRRHIDLLVGSATLCSALYVGDLGGSVFLvgQLFTfSPRRhWTTQdCNCsIYPGHI

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	123 TGHrMAWdMMNWSPTTALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
52	DK7	123 TGHrMAWdMMNWSPTTALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
59	US11	123 TGHrMAWdMMNWSPTaALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
55	DR4	123 TGHrMAWdMMNWSPTTALVVAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV
54	DR1	123 TGHrMAWdMMNWSPTTALVMAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVvVv
53	DK9	123 TGHrMAWdMMNWSPTaALVMAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVvVv
58	SW1	123 TGHrMAWdMMNWSPTTALVvAQLLRiPQAVLDmiAGAHGVLAGIAYFSMvGNWAKVLiV
57	S18	123 TGHrMAWdMMNWSPTTALViAQLLRvPQAVLDmiAGAHGVLAGIAYFSMaGNWAKVLiV
52-59	consensus	TGHrMAWdMMNWSPTtALVvAQLLRiPQaiLDmiAGAHGVLAGIAYFSMvGNWAKVLvV

FIGURE 2A

<u>SEQ ID NO:</u>	<u>Isolate</u>		
56	S14	184	LLLFAGVDA
52	DK7	184	LLLFAGVDA
59	US11	184	LLLFAGVDA
55	DR4	184	LLLFAGVDA
54	DR1	184	LLLFAGVDA
53	DK9	184	LLLFtGVDA
58	SW1	184	LLLFsGVDA
57	S18	184	LLLFaGVDA
52-59	consensus		LLLFaGVDA

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FIGURE 2B

SEQ ID NO:	Isolate	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVFEaAdlIMHTPGCVPCVREgNsSRCWVALTPTLAARNtS
62	DK1	1 YEVRNVSGvYHVTNDCSNSSIVYEAaDvIMHTPGCVPCVRENNhSRCWVALTPTLAARNAS
64	HK4	1 hEVhNVSGiYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
76	US6	1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
68	IND8	1 YEVRNVSGvYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENgfSsCWVALTPTLAARNAS
67	IND5	1 YEVRNVSGvYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
73	SW2	1 YEVRNVSGvYHVTNDCSNSSIVYETADMIMHTPGCVPCVREaNSSRCWVALTPTLAARNtS
63	HK3	1 YEVRNVSGiYHVTNDCSNSSvVYETADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNVS
66	HK8	1 YEVRNVSGiYHVTNDCSNSSIVYETADMIMHTPGcmPCVRENNSSRCWVALTPTLAARNVS
61	D3	1 YEVRNVSGvYqVTNDCSNSSIVYETADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNsS
74	T3	1 YEVRNVSGvYyVTNDCSNSSIVYETADMIMHTPGCVPCVREsNSSRCWVALTPTLAARNAS
65	HK5	1 YEVRNVSGvYHVTNDCSNlSIVYETtDMIMHTPGCVPCVRENNSSRCWVALaPTLAARNAS
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVYEAaDvIlHTPGCVPCVRENNSSRCWVALTPTLAARNSS
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
69	P10	1 YEVRNVSGvYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
60	D1	1 YEVRNVSGvYHVTNDCSNSSIVYEtADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNgn
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVYEAaDvIMHTPGCVPCVqEgNSSqCWVALTPTLAARNat
60-76	consensus	yEVrNVSGvYhVTNDCSNsSiVyEaaDmImHTPGCVPCVrEnNsSrCWVALtPTLAARNas

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FIGURE 2B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	62 vPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETlQDCNCsIYPGHl
62	DK1	62 IPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETaQDCNCsIYPGHV
64	HK4	62 IPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
76	US6	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLiSQLFTFSPPRqHETVQDCNCsIYPGHV
68	IND8	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
67	IND5	62 VsTTTIRrhVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
73	SW2	62 VPTTTIRRHVDLLVGAAAFCSvMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
63	HK3	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
66	HK8	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
61	D3	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQeCNCsIYPGHV
74	T3	62 VPTkTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
65	HK5	62 VPTTaIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
71	S45	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRHETVQDCNCsIYPGHV
72	SA10	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDL CGSVFLVSQLFTFSPPRrYETVQDCNCsIYPGrV
69	P10	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDL CGSVlLVSQLFTFSPPRHwTVQDCNCsIYPGHV
60	D1	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDL CGSVFLiSQLFTlSPRRHETVQeCNCsIYPGHV
70	S9	62 VPTTtIRRHVDLLVGAAvFCSAMYVGDL CGSVFLiSQLFTiSPRRHETVQnCNCsIYPGHV
60-76	consensus	vpTtTIRrhVDLLVGAAaFCSaMYVGDL CGSVfLVSQLFTfSPRRheTVQDCNCsIYPGHv

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FIGURE 2B

SEQ ID NO:	Isolate	
75	T10	123 SGHRMAWDMMMNWSPTTALVvSQLLRIPQAVmDMVtGAHWGVLAGLAYYSMAGNWAKVLI
62	DK1	123 SGHRMAWDMMMNWSPTTALVlSQLLRIPQAVvDMVAGAHWGVLAGLAYYSMAGNWAKVLI
64	HK4	123 SGHRMAWDMMMNWSPTAALVVSQLLRlPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
76	US6	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
68	IND8	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLI
67	IND5	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLI
73	SW2	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
63	HK3	123 SGHRMAWDMMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
66	HK8	123 SGHRMAWDMMMNWSPTtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLI
61	D3	123 TGHRMAWDMMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
74	T3	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
65	HK5	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
71	S45	123 TGHRMAWDMMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
72	SA10	123 TGHRMAWDMMMNWSPTtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLI
69	P10	123 sGHRMAWDMMMNWSPTaALVVSQLLRIPQAIldvVAGAHWGVLAGLAYYSMVGNWAKVLI
60	D1	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
70	S9	123 TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
60-76	consensus	sGHRMAWDMMMNWSPTaALVvSQLLRiPQAVvDmVaGAHWGvLAGLAYYSMvGNWAKVLI

FIGURE 2B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG
62	DK1	184 lLLFAGVDG
64	HK4	184 mLLFAGVDG
76	US6	184 lLLFAGVDG
68	IND8	184 MLLFAGVDG
67	IND5	184 MLLFAGVDG
73	SW2	184 MLLFAGVDG
63	HK3	184 MLLFAGVDG
66	HK8	184 MLLFAGVDG
61	D3	184 MLLFAGVDG
74	T3	184 lLLFAGVDG
65	HK5	184 MLLFAGVDG
71	S45	184 MLLFAGVDG
72	SA10	184 MLLFAGVDG
69	P10	184 MLLFAGVDG
60	D1	184 MLLFAGVDG
70	S9	184 MLLFAGVDG
60-76	consensus	mLLFAGVDG

FIGURE 2C

<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	1 A QVrNTsrgYMTNDCSNeSITWQLQAAVLHVPGCiPCErLGNTSRCWIPVtPNVAVRQPG
78	T4	1 A QVKNTtnSYMTNDCSNDsITWQLQAAVLHVPGCVPCEktGNTSRCWIPVSPNVAVRQPG
79	T9	1 AeVKNTSTSYMTNDCSNDsITWQLQAAVLHVPGCVPCErVGNaSRCWIPVSPNVAVRQPG
80	US10	1 vqVKNTSTSYMTNDCSNDsITWQLaAAVLHVPGCVPCEkVGntSRCWIPVSPNVAVRQPG
77-80	consensus	aqVKNtstsYMTNDCSNDsITWQLqAAVLHVPGCvPCE-vGntSRCWIPVsPNVAV--PG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSPrrHWFVQeCNCSIYPGTI
78	T4	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSPQHHWFVQdCNCSIYPGTI
79	T9	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIiSPQHHWFVQECNCSIYPGTI
80	US10	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSPrHHSFVQECNCSIYPGTI
77-80	consensus	ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMLAAQMFIvSP-hHwFVQeCNCSIYPGTI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	123 TGHrMAWDMMNWSPTATMILAYAMRVPEVIiDIigGAHWGVmFGLAYFSMQAWAKViVi
78	T4	123 TGHrMAWDMMNWSPTATMILAYAMRVPEVIldIvSGAHWGVmFGLAYFSMQAWAKVVVI
79	T9	123 TGHrMAWDMMNWSPTtTMILAYAMRVPEVIIDIISGAHWGVmFGLAYFSMQAWAKVVVI
80	US10	123 TGHrMAWDMMNWSPTaTlILAYvMRVPEVIIDIISGAHWGVlFGLAYFSMQAWAKVVVI
77-80	consensus	TGHrMAWDMMNWSPTaTmILAYaMRVPEVIiDIISGAHWGVmFGLAYFSMQAWAKVvVI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	184 LLLAAGVDA
78	T4	184 LLLAAGVDA
79	T9	184 LLLtAGVDA
80	US10	184 LLLaAGVDA
77-80	consensus	LLLaAGVDA

FIGURE 2D

SEQ ID NO: Isolate

82 DK11

83 SW3

84 T8

81 DK8

81-84 consensus

1 VEVNRtSSSYATNDCSNnSITWQLTNAVHLHLP GCVP CENDNGTLHCW IQVTPNVAVKH RG
 |||||
 1 VEVRNiSSSYATNDCSNnSITWQLTNAVHLHLP GCVP CENDNGTLHCW IQVTPNVAVKH RG
 |||||
 1 VEVNRtSfSYATNDCSNnSITWQLTNAVHLHLP GCVP CENDNGTLRCW IQVTPNVAVKH RG
 |||||
 1 VEVRNiSsSYATNDCSNnSITWQLTNAVHLHLP GCVP CENDNGTLRCW IQVTPNVAVKH RG
 |||||
 VEVRN-SsSYATNDCSNnSITWQLTNAVHLHLP GCVP CENDNGTL-CW IQVTPNVAVKH RG

SEQ ID NO: Isolate

82 DK11

83 SW3

84 T8

81 DK8

81-84 consensus

62 ALTHNLRahIdMIVMAATVCSALYVG DvCGAVMIVSQAFIvSPEhHhFTQECNC SIYQGH I
 |||||
 62 ALTHNLRahVdMIVMAATVCSALYVG DmCGAVMIVSQAFIISPERHNFTQECNC SIYQG rI
 |||||
 62 ALTHNLRTHVDVIVMAATVCSALYVG DVCGAVMIaSQAFIISPERHNFTQECNC SIYQGH I
 |||||
 62 ALTHNLRTHVDVIVMAATVCSALYVG DVCGAVMIvSQAlIISPERHNFTQECNC SIYQGH I
 |||||
 ALTHNLR-HvD-IVMAATVCSALYVG DvCGAVMIvSQAFIISPERHnFTQECNC SIYQGH I

SEQ ID NO: Isolate

82 DK11

83 SW3

84 T8

81 DK8

81-84 consensus

123 TGHRMAWDMMLNWSPTLTMI LAYAA RVP ELVLEV VFGGHWGVVFG LAYFSMQGAWAKVIAI
 |||||
 123 TGHRMAWDMMLNWSPTLTMI LAYAA RVP ELVLEV VFGGHWGVVFG LAYFSMQGAWAKVIAI
 |||||
 123 TGHRMAWDMMLNWSPTLTMI LAYAA RVP ELVLEV VFGGHWGVVFG LAYFSMQGAWAKVIAI
 |||||
 123 TGHRMAWDMMLNWSPTLTMI LAYAA RVP ELaLqVVFGGHWGVVFG LAYFSMQGAWAKVIAI
 |||||
 TGHRMAWDMMLNWSPTLTMI LAYAA RVP ELvLeVVFGGHWGVVFG LAYFSMQGAWAKVIAI

SEQ ID NO: Isolate

82 DK11

83 SW3

84 T8

81 DK8

81-84 consensus

184 LLLVAGVDA
 |||||
 184 LLLVAGVDA
 |||||
 184 LLLVAGVDA
 |||||
 184 LLLVAGVDA
 |||||
 LLLVAGVDA

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FIGURE 2E

SEQ ID NO: Isolate

86 DK12

87 HK10

88 S2

90 S54

89 S52

86-90 consensus

1 LEWRNVSGLYVLTNDCsNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSTPTVAVRYVG
 |||||
 1 LEWRNVSGLYVLTNDCpNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSTPTVAVRYVG
 |||||
 1 LEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTPTPTVAVRYVG
 |||||
 1 LEWRNTSGLYiLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTPTPTVAVRYVG
 |||||
 1 LEWRNTSGLYvLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSmCWTPTPTVAVRYVG
 |||||
 LEWRNtSGLYvLTNDCsNSSIVYEADDVILHTPGCVPCVQDGNTStCWTpVTPTVAVRYVG

SEQ ID NO: Isolate

86 DK12

87 HK10

88 S2

90 S54

89 S52

86-90 consensus

62 ATTASIRSHVDLLVGAATMCSALYVGDvCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
 |||||
 62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
 |||||
 62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
 |||||
 62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
 |||||
 62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHv
 |||||
 ATTASIRSHVDLLVGAATmCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL

SEQ ID NO: Isolate

86 DK12

87 HK10

88 S2

90 S54

89 S52

86-90 consensus

123 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTLFDIiAGAHWGImAGLAYYSMQGNWAKVAII
 |||||
 123 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTLFDIiAGAHWGILAGLAYYSMQGNWAKVAII
 |||||
 123 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTVFDIiAGAHWGILAGLAYYSMQGNWAKVAII
 |||||
 123 SGHRMAWDMMNWSPAVGMVVAHILRPLPQTLFDIiAGAHWGILAGLAYYSMQGNWAKVAII
 |||||
 123 SGHRMAWDMMNWSPAVGMVVAHILRPLPQTLFDIiAGAHWGILAGLAYYSMQGNWAKVAIv
 |||||
 SGHRMAWDMMNWSPAVGMVVAHVLRPLPQTLFDIiAGAHWGILAGLAYYSMQGNWAKVAii

SEQ ID NO: Isolate

86 DK12

87 HK10

88 S2

90 S54

89 S52

86-90 consensus

184 MVMFSGVDA
 |||||
 184 MVMFSGVDA
 |||||
 184 MVMFSGVDA
 |||||
 184 MIMFSGVDA
 |||||
 184 MIMFSGVDA
 |||||
 MvMFSGVDA

FIGURE 2F

SEQ ID NO: Isolate

94 27

93 26

93-94 consensus (Z6)

1 VNYhNASGVYHlTNDCPNSSImYEAEHhILHLPGCVPVReGNQSRCWVALTPTVAAPYIG
|||
1 VNYrNASGVYHvTNDCPNSSiVYEAHqILHLPGLPCVrvGNQSRCWVALTPTVAvsYIG
VNYrNASGVYHvTNDCPNSSiVYEAHqILHLPGLPCVrvGNQSRCWVALTPTVAvsYIG

SEQ ID NO: Isolate

94 27

93 26

93-94 consensus (Z6)

62 APLESiRRHVDLMVGAATVCSALYIGDLCGGVFLVGQMFsfQPRRHWTtQDCNCsIYAGHV
 62 APLdSLRRHVDLMVGAATVCSALYvGDLCGgaFLVGQMFsfQPRRHWTtQDCNCsIYAGHI
 APLdSLRRHVDLMVGAATVCSALYvGDLCGgaFLVGQMFsfQPRRHWTtQDCNCsIYAGHi

SEQ ID NO: Isolate

94 27

93 26

93-94 consensus (26)

123 TGHRMAWDMMMNSPTTTLvLAQVMRIPSTLVDLLTGHHWGILiGvAYFcMQANWAKVILV
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
123 TGHRMAWDMMMNSPTTTLlLAQVMRIPSTLVDLLAGGHWGvLVGLAYFSMQANWAKVILV
TGHRMAWDMMMNSPTTTLlLAQVMRIPSTLVDLLaGGHWGvLvGLAYFsMQANWAKVILV

SEQ ID NO: Isolate

94 27

93 26

93-94 consensus (Z6)

```

184  LFLyAGVDA
      ||| |||||
184  LFLFAGVDA
      ||| |||||
      LFLfAGVDA

```

FIGURE 2G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVkegNVSRCWVQITPTLSAPNLG
100	SA7	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQnNVSRCWVQITPTLSAPNLG
97	SA4	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQDNVSkCWVQITPTLSAPNLG
96	SA1	1 VPYRNASGVYHVTNDCPNSSIVYEADsLILHAPGCVPCVRQDNVSRCWVQITPTLSAPtfg
99	SA6	1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRkDNVSRCWVhITPTLSAPSLG
101	SA13	1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRqgNVSRCWVqITPTLSAPSLG
96-101	consensus	VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVPCVrqdNVSRcWVqITPTLSAPnlg

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	62 AVTAPLRRvVDYLAGGAALCSALYVGDACGAVFLVGQMFtYRPRQHTTVQDCNCISIYSGHI
100	SA7	62 AVTAPLRRAVDYLGAALCSALYVGDACGAVFLVGQMFsYRPRQHTTVQDCNCISIYSGHI
97	SA4	62 AVTAPLRRAVDYLGAALCSALYVGDACGAVFLVGQMFTYRPRQHTTVQDCNCISIYSGHI
96	SA1	62 AVTAPLRRAVDYLGAALCSALYVGDACGAVFLVGQMFTYRPRQHTTVQDCNCISIYSGHI
99	SA6	62 AVTAPLRRAVDYLGAALCSALYVGdvCGAlFLVGQMFTYRPRQHaTVQDCNCISIYSGHI
101	SA13	62 AVTAPLRRAVDYLGAALCSALYVGDaCGAvFLVGQMFTYsPRrHnvVQDCNCISIYSGHI
96-101	consensus	AVTAPLRRaVDYLAGGAALCSALYVGDaCGAvFLVGQMFtYrPRqHttVQDCNCISIYSGHI

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	123 TGHMAWDMMMNWSPTTALVMAQvLRIPQVVIDIIAGGHWGVLFaVAYFASAANWAKVVLV
100	SA7	123 TGHMAWDMMMNWSPTTALVMAQLLRIPQVVIDIIAGGHWGVLFaaYFASAANWAKVVLV
97	SA4	123 TGHMAWDMMMNWSPTTALLMAQLLRIPQVVIDIIAGGHWGVLFaaYFASAANWAKViLV
96	SA1	123 TGHMAWDMMMNWSPTTALLMAQMLRIPQVVIDIIAGGHWGVLFaaYFASAANWAKVVLV
99	SA6	123 TGHMAWDMMMNWSPaTALVMAQMLRIPQVVIDIIAGGHWGVLFaaYFASAANWAKVVLV
101	SA13	123 TGHMAWDMMMNWSPtTALVMAQlLRIPQVVIDIIAGaHWGVLFaaYyASAANWAKVVLV
96-101	consensus	TGHMAWDMMMNWSPtTALvMAQlLRIPQVVIDIIAGgHWGVLFaaYfASAANWAKVvLV

FIGURE 2G

<u>SEQ ID NO:</u>	<u>Isolate</u>		
98	SA5	184	LFLFAGVDg
100	SA7	184	LFLFAGVDA
97	SA4	184	LFLFAGVDA
96	SA1	184	LFLFAGVDg
99	SA6	184	LFLFAGVDA
101	SA13	184	LFLFAGVDA
96-101	consensus		LFLFAGVDA

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FIGURE 2H

SEQ ID NO: Genotype
 81-84 (IV/2b)
 (2c)
 77-80 (III/2a)
 86-90 (V/3a)
 60-76 (II/1b)
 52-59 (I/1a)
 (4a)
 93-94 (4c)
 (4d)
 (4b)
 96-101 (5a)
 (6a)
 52-102 consensus

1 VEVrNiSsSYATNDCSNnSITWQLTnAVLHLPgcVPCENDNGTLrCWIQVTPNVAVKHRC
 1 VEVKDTGDSYMPNTDCSNSSIVWQLEGAVLHTPGCVPCERTANVSRCWVPVAPNLAI SQPC
 1 aqVknTstSYMTNDCSNdsITWQLqAAVLHVPgcVPCekvGntSRCWIPVsPNVAVqqPC
 1 LEWRntSGLYvLTNDCSNssIVYEADDVILHTPGCVPCVQDGNtStCWTPVTPTVAVRYVQ
 1 yEVrNVSGvYhVTNDCSNesIVyEaaDmImHTPGCVPCVrEnNsSrCWVALtPTLAARNaS
 1 yQVRNStGLYHVTNDCPNSSIVYEaADaILHsPGCVPCVREgnasrCWVavtPTVATRDGK
 1 EHYRNASGIYHITNDCPNSSIVYEADHHILHLPgcVPCVMTGNtSRCWTPVTPTVAVAHPC
 1 VNYrNASGVYHvTNDCPNSSIVyEAHqILHLPgcVPCVrVnQSRCWVALTPTVAVsYIC
 1 YNYRNSSGVYHVTNDCPNSSIVyETDYHILHLPgcVPCVREGNKStCWVSLTPTVAAQHNLN
 1 VHYRNASGVYHVTNDCPNTSIVyETEHIMHLPgcVPCVrTENTSRCWVPLTPTVAAYPNP
 1 VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVPVrqqDNVsrCWVqITPTLSAPnLG
 1 LTYGNSSGLYHLTNDCPNSSIVLEADAMILHLPgcVPCVrVDDRSTCWHAVTPTLAIPNAS

 Y TNDC N S H PGC PC CW P

SEQ ID NO: Genotype
 81-84 (IV/2b)
 (2c)
 77-80 (III/2a)
 86-90 (V/3a)
 60-76 (II/1b)
 52-59 (I/1a)
 (4a)
 93-94 (4c)
 (4d)
 (4b)
 96-101 (5a)
 (6a)
 52-102 consensus

62 ALTHNLrHvDmIVMAATVCSALYVGdVCGAVMIvSQAfIiSPeRhnFTQECNCSiYQGHl
 62 ALTkGLRAHIDIIVMSATVCSALYVGdVCGALMLAAQVVVSPQHHTFVQECNCSiYPGRl
 62 ALTQGLRTHIDMVMSATLCSALYVGdLcGGvMLAAQMFIvSPqhHwFVQeCNCSiYPGTI
 62 ATTASIRSHVDLLVGAAmCSALYVGdMCGAVFLVGQAFTFRPRRHQTvQTCNCSLYPGHl
 62 vpTttIRrHVDLLVGAAaFCSaMYVGdLcGSvFLvSQLFTfSPRrheTvQdCNCSiYPGHv
 62 LPatQLRRhIDLLVGSATLCSALYVGdLcGSvFLvSQLFTfSPRrheTvQdCNCSiYPGHv
 62 APLESFRRHVDLMVGAATLCSALYVGdLcGGaFLMGQMITFRPRRHWTtQdCNCSiYPGHl
 62 APLdsLRRHVDLMVGAATVCSALYvGDLCGGaFLVGQMFsFQPRRHWTtQdCNCSiYAGHi
 62 APLESRRHVDLMVGGATLCSALYIGdVCGGVFLVGQLFTFQPRRHWTtQdCNCSiYTGHl
 62 APLESRRHVDLMVGAATMCSAFYIGdLcGGvFLVGQLFDfRPRRHWTtQdCNCSiYPGHV
 62 AVTAPLRRaVDYLAGGAALCSALYVGdACGAvFLVGQMFtYrPRqHttVQDCNCSiYSGHl
 62 TPATGFRRHVDLLAGAAVVCSSLYIGdLcGSFLAGQLFTFQPRRHWTtQdCNCSiYTGHV

 R D A CS Y GD CG Q P Q CNCS Y G

SEQ ID NO: Genotype
 81-84 (IV/2b)
 (2c)
 77-80 (III/2a)
 86-90 (V/3a)
 60-76 (II/1b)
 52-59 (I/1a)
 (4a)
 93-94 (4c)
 (4d)
 (4b)
 96-101 (5a)
 (6a)
 52-102 consensus

123 TGHRMAWDMMLNWSPTLTmILAYAArVPELvLeVVFGGHWGVVFGLAYFSMQGAWAKVIAI
 123 TGHRMAWDMMNWSPTTTMLLAYLVRIPEVILDIvTGGHGWGMFGLAYFSMQGSWAKVIVI
 123 TGHRMAWDMMNWSPTaTmILAYaMRVPEVIIdIIsGAHWGVmFGLAYFSMQGAWAKVvVI
 123 SGHRMAWDMMNWSPAVGMVVAHvLRLPQTlFDIiAGAHWGIlAGLAYFSMQGNWAKVAIi
 123 sGHRMAWDMMNWSPTaALVvSQLLRiPQAvvDmVaGAHWGvLAGLAYFSMvGNWAKVLIV
 123 TGHRMAWDMMNWSPTtALVvAQLLRiPQAIldMIAGAHWGvLAGIAYFSMvGNWAKVLvV
 123 TGHRMAWDMMNWSPTTTLLLAQIMRVPTAFldMVAGGHGWGLAGLAYFSMQGNWAKVVLV
 123 TGHRMAWDMMNWSPTATLVLAQLMRIPGAMVDLLAGGHWGIlVGIAIFSMQANWAKVILV
 123 SGHRMAWDMMNWSPTSALIMAQILRIPSILGDLLTGGHGWGLAGLAFFSMQSNWAKVILV
 123 TGHRMAWDMMNWSPTaLvmAQlLRIPQVVIDIiAGqHWGVLFaaAYfASAANWAKVvLV
 123 TGHRMAWDMMNWSPTTTLVLSSILRVPEICASVIFGGHWGILLAVAYFGMAGNWLKVLA

 GHRMAWDM NWSP R P G HWG A W KV

FIGURE 2H

<u>SEQ ID NO:</u>	<u>Genotype</u>		
81-84	(IV/2b)	184	LLLVAGVDA
85	(2c)	184	LLLTAGVEA
77-80	(III/2a)	184	LLLaAGVDA
86-90	(V/3a)	184	MvMFSGVDA
60-76	(II/1b)	184	mLLFAGVDG
52-59	(I/1a)	184	LLLFaGVDA
91	(4a)	184	LFLFAGVDA
93-94	(4c)	184	LFLfAGVDA
95	(4d)	184	LFLFAGVDA
92	(4b)	184	LFLFAGVEG
96-101	(5a)	184	LFLFAGVDa
102	(6a)	184	LFLFAGVEA
52-102	consensus		GV

09034691 052698

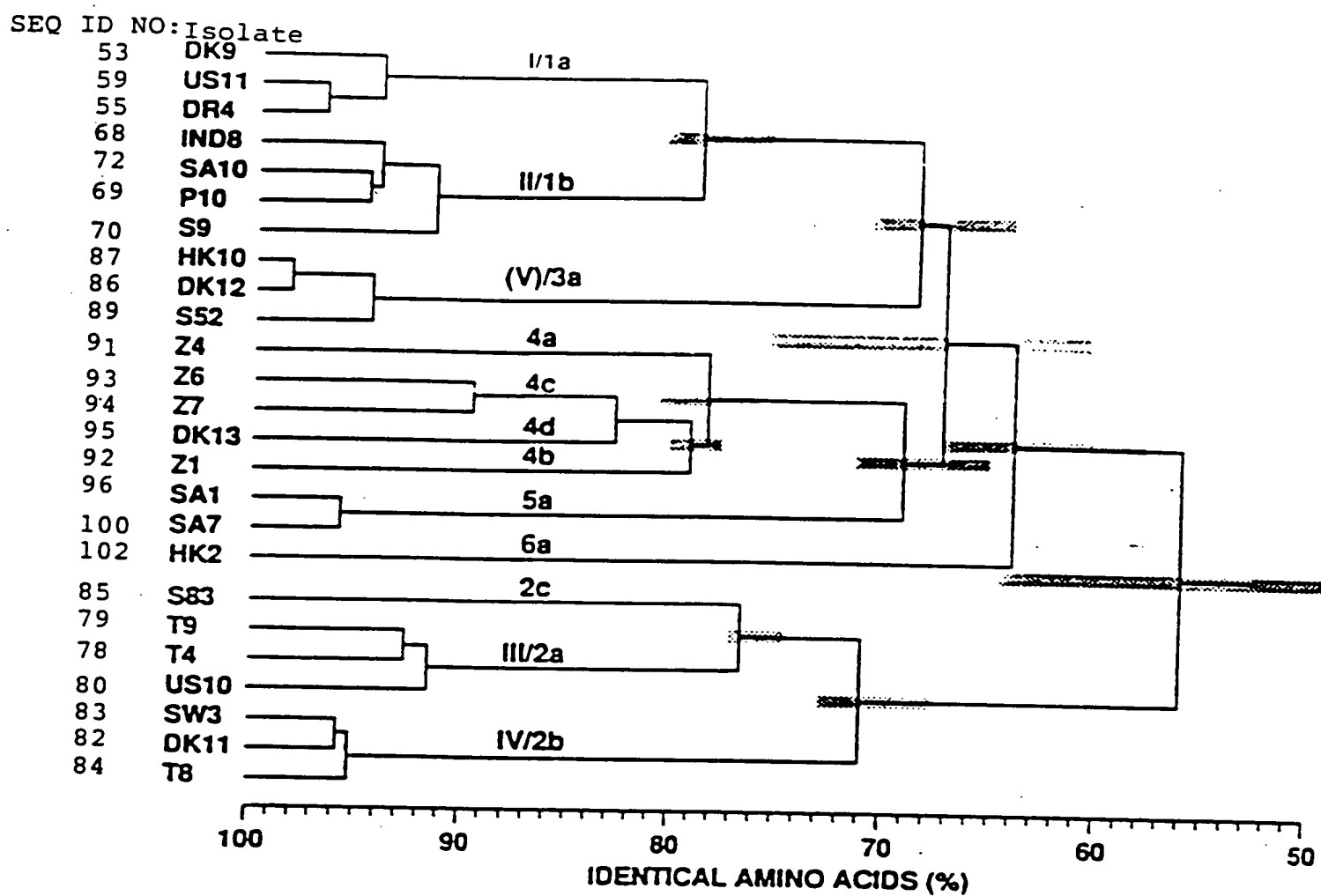
FIGURE 3

Genotype	SEQ ID NO: 52-102	Isolate	yevrnvgvYhvtNDcNSsiyyeaadailHtPGCvPvregntsrCwvavtPtvaaarnagaptttLRihvDillvgaALCSalyvGDICGsvflv
IV/2b	82	DK11	VEVRNtSSS-YA---S-n-ITWOLTNAVL-L---V-ENdNGTLH-IOVT-NVAVRHGALTHNL-AHI-MIVMA-TV-AL-V-v-AVMIV
	83	SW3	VEVRNtSSS-YA---S-b-ITWOLTNAVL-L---V-ENdNGTLH-IOVT-NVAVRHGALTHNL-AHV-MIVMA-TV-AL-V-m-AVMIV
	81	DK8	VEVRNtSSS-YA---S-N-ITWOLTNAVL-L---V-ENdNGTLR-IOVT-NVAVRHGALTHNL-THV-MIVMA-TV-AL-V-v-AVMIV
	84	T8	VEVRNtSSS-YA---S-N-ITWOLTNAVL-L---V-ENdNGTLR-IOVT-NVAVRHGALTHNL-THV-MIVMA-TV-AL-V-v-AVMIV
2c	85	S83	VEVRNtSSS-Mp---S-b-IVMOLegAVL-t---V-ErTanvSR-vpva-NIaISOPGALTkGL-aHI-IIVMS-TV-AL-V-v-AIMLA
	78	T4	aQVKNtNS-MV---S-D-ITWOLGAALV-L---V-EKtGNtSR-IPVS-NVAVRHGALThQGL-THI-MVMS-TL-AL-V-l-GvMLA
	80	US10	aQVKNtNS-MV---S-D-ITWOLGAALV-L---V-EKtGNtSR-IPVS-NVAVRHGALThQGL-THI-MVMS-TL-AL-V-l-GvMLA
	79	T9	aQVKNtNS-MV---S-D-ITWOLGAALV-L---V-EKtGNtSR-IPVS-NVAVRHGALThQGL-THI-MVMS-TL-AL-V-l-GvMLA
(V) /3a	77	T2	aQVKNtNS-MV---S-e-ITWOLGAALV-L---V-ERIGNtSR-IPVT-NVAVRHGALThQGL-THI-MVMS-TL-AL-V-l-GvMLA
	86	DK12	LEVRNtSGL-VL---S-S-IVYEADDDVIL-T---V-VODGNtST-TSPT-TVAVRVGGATTASI-SHV-LLVGA-TM-AL-V-v-AVFLV
	87	HK10	LEVRNtSGL-VL---S-S-IVYEADDDVIL-T---V-VODGNtST-TSPT-TVAVRVGGATTASI-SHV-LLVGA-TM-AL-V-v-AVFLV
	88	S2	LEVRNtSGL-VL---S-S-IVYEADDDVIL-T---V-VODGNtST-TSPT-TVAVRVGGATTASI-SHV-LLVGA-TM-AL-V-v-AVFLV
II/1b	90	S54	LEVRNtSGL-VL---S-S-IVYEADDDVIL-T---V-VODGNtST-TSPT-TVAVRVGGATTASI-SHV-LLVGA-TM-AL-V-v-AVFLV
	89	S52	LEVRNtSGL-VL---S-S-IVYEADDDVIL-T---V-VODGNtST-TSPT-TVAVRVGGATTASI-SHV-LLVGA-TM-AL-V-v-AVFLV
	68	IND8	YEVRNtSGV-HV---S-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	67	IND5	YEVRNtSGV-HV---S-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
I/1a	59	DR4	HOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	55	DR1	HOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	54	DR1	HOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	53	DK9	HOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
4a	58	SW1	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	56	S14	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	57	S18	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	51	24	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
4c	93	26	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	94	27	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	95	DK13	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	92	21	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
5a	98	SA5	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	100	SA7	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	97	SA4	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	96	SA1	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
6a	99	SA6	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	101	SA13	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV
	102	HK2	YOVRNtSGL-HV---P-S-IVYEADADMIM-T---V-VREGNtSR-VALT-TLAARNASvPTTTI-rHV-LLVGA-AP-AM-V-l-SVFLV

FIGURE 3

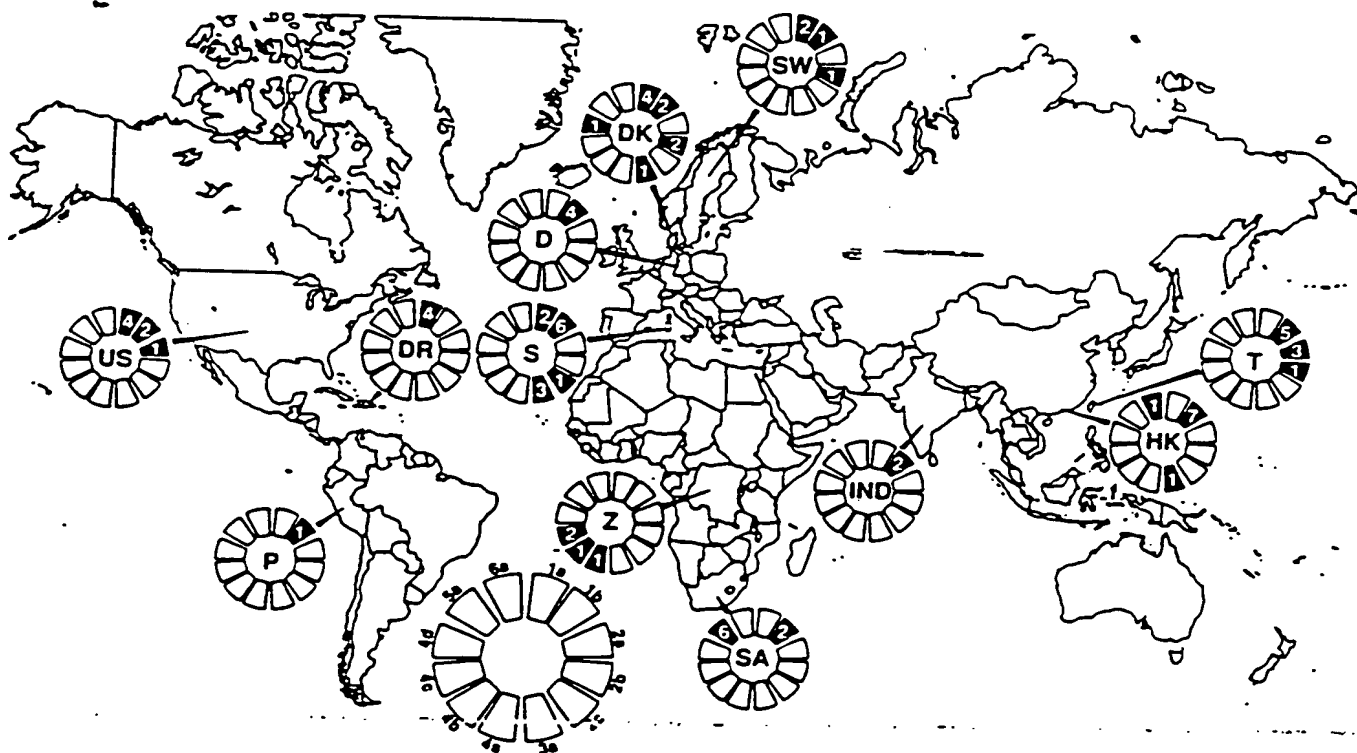
Genotype	SEQ ID NO: 52-102	Isolate	290	300	310	320	330	340	350	360	370	380
IV/2b	82	DK11	S-AFIYS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELVLEVF-G	VFGL-YFSMOGA-A	IAILLVA--DA				
	83	SW3	S-AFIIS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELVLEVF-G	VFGL-YFSMOGA-A	IAILLVA--DA				
	81	DK8	S-AFIIS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELALQVF-G	VFGL-YFSMOGA-A	IAILLVA--DA				
	84	T8	S-AFIIS-ERHhFT-E	I-Q-HIT	L	TLTMIAYAA-V-ELVLEVF-G	VFGL-YFSMOGA-A	IAILLVA--DA				
2c	85	S83	A-VVVS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIV-G	VMFGL-YFSMOGA-A	IVILLTA--ea				
	78	T4	A-MFIS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIV-G	VMFGL-YFSMOGA-A	IVILLTA--ea				
	80	US10	A-MFIS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIV-G	VMFGL-YFSMOGA-A	IVILLTA--ea				
	79	T9	A-MFIS-QHhFT-E	I-P-HIT	M	TTTMIAYV-i-EVILDIV-G	VMFGL-YFSMOGA-A	IVILLTA--ea				
(V)/3a	86	DK12	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTFLDIIA-A	IMAGL-YYSMOGN-A	AIIMVMS--DA				
	87	HK10	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTFLDIIA-A	IMAGL-YYSMOGN-A	AIIMVMS--DA				
	88	S2	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTFLDIIA-A	IMAGL-YYSMOGN-A	AIIMVMS--DA				
	90	S54	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTFLDIIA-A	IMAGL-YYSMOGN-A	AIIMVMS--DA				
II/1b	89	S52	G-AFTER-RRHhFT-E	L-P-HIT	M	AVGMVVAHV-L-OTFLDIIA-A	IMAGL-YYSMOGN-A	AIIMVMS--DA				
	68	IND8	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	67	IND5	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	73	SW2	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
I/1a	63	HK3	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	66	HK8	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	71	S45	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	61	D3	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
4a	64	HK5	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	65	HK4	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	66	US6	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	76	P10	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
4c	69	SA10	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	72	T10	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	75	DK1	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	70	S9	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
4b	60	D1	S-LFTFS-RRHhFT-E	I-P-HIT	M	TAALVWSOLL-I-OAVDMVA-A	ILAGL-YYSMOGN-A	LIVMLFA--DG				
	52	DK7	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	59	US11	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	55	DR4	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
5a	54	DR1	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	53	DK9	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	58	SW1	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	56	S14	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
6a	57	S18	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	91	Z4	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	93	Z6	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	94	Z7	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
4d	95	DK13	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	92	Z1	G-LFTFS-RRHhFT-E	I-P-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	98	SA5	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	100	SA7	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
5a	97	SA4	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	96	SA1	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	99	SA6	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
	101	SA13	G-MFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
6a	102	HK2	G-LFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				
			G-LFTFS-RRHhFT-E	I-S-HIT	M	TTTLLAQIM-V-ELVDMVA-G	VLGL-YFSMOGN-A	VLVFLFA--da				

FIGURE 4



05034591.0330

FIGURE 5



869250 " T6948060

FIGURE 6A

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG

ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG

ACGTcAAGTTCCCGGGTGGCGGTGAGATCGTTGGTGGAGTTTACTTGTGTCGCGCAGGGG

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

123 CCCTAGATTGGGTGTGCGCGCGaCGAGGAAGACTTCCGAGCGGTTCGCAACCTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGcCGAGGAAGACTTCCGAGCGGTTCGCAACCTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTTCGCAACCTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTTCGCAACCTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTTCGCAACCTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTTCGCAACCTCGcGGTAGA

CCCTAGATTGGGTGTGCGCGCGaCGAGGAAGACTTCCGAGCGGTTCGCAACCTCGaGGTAGA

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

184 CGTCAGCCTATCCCCAAGGCgCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
 184 CGTCAGCCTATCCCCAAGGCACGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
 184 CGTCAGCCTATCCCCAAGGCACGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
 184 CGTCAGCCTATCCCCAAGGCACGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
 184 CGTCAGCCTATCCCCAAGGCgCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
 184 CGTCAGCCTATCCCCAAGGCgCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC

CGTCAGCCTATCCCCAAGGC - CGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTcCCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCCCCCGTGG
 245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCCCCCGTGG

CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTc - CCCCCGTGG

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTTCGCGCAATTTGGGTAAgGTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGcAGGTTCGCGCAATTTGGGTAAaGTC
 306 CTCTCGGCCTAGCTGGGGCCCCACgGACCCCCGGCGTAGGTTCGCGCAATTTGGGTAAAGTTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTTCGCGCAATTTGGGTAAAGTTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTTCGCGCAATTTGGGTAAAGTTC
 306 CTCcCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTTCGCGCAATTTGGGcAAaGTC

CTCTcCGGCCTAGCTGGGGCCCCcACaGACCCCCGGCGtAGGTTCGCGCAATTTGGGtAAgGTC

FIGURE 6A

SEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

367 ATCGA~~c~~ACCCT~~c~~ACGTGCGGCTTCGCCGACCTCATGGGGTACAT~~c~~CCGCTCGTCGGCGCCC
367 ATCGATAACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
367 ATCGATAACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
367 ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
367 ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
367 ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC

ATCGA~~t~~ACCCT~~c~~ACGTGCGGCTTCGCCGACCTCATGGGGTACAT~~a~~CCGCTCGTCGGCGCCCSEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

428 C~~c~~CTTG~~g~~GGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG~~a~~GTTCTGGAAGACGGCGTGAA
428 CTCTTGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 CTCTCGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 C~~c~~CTCG~~g~~GGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 CTCT~~t~~GGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 CTCT~~c~~GGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA

C~~t~~CT-~~G~~GaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG~~g~~GTTCTGGAAGACGGCGTGAASEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

489 CTATGCAACAGGGA~~t~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGC~~t~~tTGCTCTCT
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCCCTGCTCTCT
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCCCTGCTCTCT
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCT~~t~~cTaGCCCTGCTTTCT
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCCCTGCTTTCT
489 CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCCCTGCT~~t~~TCT

CTATGCAACAGGGA~~a~~CTTCCTGGTTGCTCTTTCTCTATCTTCCT~~t~~cTgGC~~c~~cTGCT~~t~~TCTSEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

550 TG~~c~~tTGACCGTGCCCGCaTCGGCC
550 TGCCTGACCGTGCCCGCTTCGGCC
550 TGCCTGACTGTGCCCGCTTCAGCC
550 TGCCTGACTGTGCCCGCTTCAGCC
550 TGCCTGACaGTGCCCGCGTCAGCC
550 TG~~t~~CTGAC~~t~~GTGCCCGCGTCAGC~~t~~

TG~~c~~cTGAC~~t~~GTGCCCGC~~t~~TCaGCC

09034551 052659

FIGURE 6B

SEQ ID NO:	ISOLATE	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
118	IND8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
116	SW2	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
122	HK4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAgACCAAACGTAACACCAACCGCCGCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAAGAcAAACCAAACGTAACACCAACCGCCGCCACAGG
123	P8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAAGCCGCCGCCACAGG
124	T3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
121	HK5	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
109-124	consensus	ATGAGCACGAATCCTAAACCTCAAAGAAaAaACCAAACGTAACACCAaCCGCCGCCACAGG
119	S9	62 ACGTtAAGTTCCCGGGCGGTGGtCAGATCGTcGGTGGAGTTTACCTGTTGCCGCGCAGGGG
117	IND3	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
118	IND8	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
111	D1	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
112	US6	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
113	P10	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
114	DK1	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
115	T10	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
116	SW2	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
122	HK4	62 ACGTtAAGTTCCCGGGCGGTGGCCAGATCGTcGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109	SA10	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTtTaTcTGTGTTGCCGCGCAGGGG
110	S45	62 ACGTCAAGTTCCCGGGtGGcGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
123	P8	62 ACGTtAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
124	T3	62 ACGTtAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
120	HK3	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
121	HK5	62 ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109-124	consensus	ACGTcAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTaCCTGTTGCCGCGCAGGGG
119	S9	123 CCCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
117	IND3	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
118	IND8	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
111	D1	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
112	US6	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
113	P10	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
114	DK1	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
115	T10	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
116	SW2	123 CCCCcGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
122	HK4	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
109	SA10	123 CCCCAGGTTGGGTGTGCGCGCGAcgAGGAAGACTTCCGAGCGGTTCGCAACCTCGTGGAAGG
110	S45	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTTCaCAACCTCGTGGAAGG
123	P8	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCaCAACCTCGTGGAAGG
124	T3	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
120	HK3	123 CCCCAGGTTGGGTGTGCGCGCGGACCAGGAAGACTTcAGAGCGGTTCGCAACCTCGTGGAAGG
121	HK5	123 CCCCAGGTTGGGTGTGCGCGCGGACCAGGAAGACTTCCgAGCGGTTCGCAACCTCGTGGAAGG
109-124	consensus	CCCCaGGTTGGGTGTGCGCGCgACTAGGAAGACTTCCgAGCGgTCgCAACCTCGTGGAAGG
119	S9	184 CGACAACCTATCCCCAAGGCTCGCCatCCCGAGGGcAGGGCCTGGGCTCAGCCCGGGTACC

FIGURE 6B

117	IND3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
118	IND8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGcACC
111	D1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
112	US6	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
113	P10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
114	DK1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
115	T10	184	CGACA _g CCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
116	SW2	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCctGGGTACC
122	HK4	184	CGACAACCTATCCCCAAGGCTCGCCa _g CCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
109	SA10	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
110	S45	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
123	P8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGCACC
124	T3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
120	HK3	184	CGACAACCTATCCCCAAGGCTCGCCa _g CCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
121	HK5	184	CGACAACCTATCCCCAAGGCTCGCC _g ACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC

109-124 consensus

CGACAaCCTATCCCCAAGGCTCGCC_ggCCCGAGGGcAGG_gCCTGGGCTCAGCCcGGGtAcCSEQ ID NO: ISOLATE

119	S9	245	CTTGGCCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGtGG
117	IND3	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
118	IND8	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
111	D1	245	CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
112	US6	245	CTTGGCCCCCTCTATGGCAACGAGGGc _a TGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
113	P10	245	CTTGGCCCCCTCTATGGCAATGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
114	DK1	245	CTTGGCCCCCTCTATGGCAATGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGcGG
115	T10	245	CTTGGCCCCCTCTATGGCAATGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGtGG
116	SW2	245	CcTGGCCCCCTCTATGGCAATGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
122	HK4	245	CTTGGCCCCCTCTATGGCAATGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCcCCCCGCGG
109	SA10	245	CTTGGCCCCCTCTATGGCAATGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
110	S45	245	CTTGGCCCCCTCTATGGCAATGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
123	P8	245	CTTGGCCCCCTCTATGcCAATGAGGGc _t TGGGGTGGGCgGGATGGCTCCTGTCACCCCGCGG
124	T3	245	CTTGGCCCCCTCTATGGc _g ACGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
120	HK3	245	CTTGGCCCCCTCTATGGCAACGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
121	HK5	245	CTTGGCCCCCTCTATGGCAAtGAGGGc _t TGGGGTGGGCAGGATGGCTCCTGTCACCCcAtGG

109-124 consensus

CtTGGCCCCCTCTAtG_gCaAtGAGGGC - TGGG_gTGGGCaGGATGGCTCCTGTCaCCCCgCGGSEQ ID NO: ISOLATE

119	S9	306	cTCTCGGCCTAGTTGGGGCCCCAatGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
117	IND3	306	tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
118	IND8	306	CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
111	D1	306	CTCCCGGCCTAGTTGGGGCCCCACcGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
112	US6	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
113	P10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
114	DK1	306	CTCTCGGCCTAGTTGGGGCCCCAa _c GACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
115	T10	306	CTCcCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
116	SW2	306	CTCTCGGCCTAGTTGGGGCCCCAc _t GACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
122	HK4	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
109	SA10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGtAATTTGGGTAAGGTC
110	S45	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
123	P8	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
124	T3	306	CTCCCGGCCTAATTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGtAATcTGGGTAAGGTC
120	HK3	306	CTCTCGGCCTAATTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
121	HK5	306	CTCTCGGCCTAgTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGtAATTTGGGTAAGGTC

109-124 consensus

cTCTCGGCCTAgTTGGGGCCCCAc_gGACCCCCGGCGTAGGTCGCGtAATtTGGGTAAGGTCSEQ ID NO: ISOLATE

119	S9	367	ATCGATACCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCC
117	IND3	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
118	IND8	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC

FIGURE 6B

111	D1	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
112	US6	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
113	P10	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
114	DK1	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
115	T10	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
116	SW2	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
122	HK4	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
109	SA10	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
110	S45	367	ATCGATAACCCTCACgTGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
123	P8	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGgCC
124	T3	367	ATCGATAACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCtC
120	HK3	367	ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGtGCCC
121	HK5	367	ATCGATAACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGcGCCC
109-124 consensus			ATCGATAACCCTCACaTGCGGCTTCGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc

SEQ ID NO:	ISOLATE	
119	S9	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
117	IND3	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA
118	IND8	428 CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA
111	D1	428 CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
112	US6	428 CCCTAGGGGGCGCTGCCAGGGCctTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
113	P10	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA
114	DK1	428 CCCTAGGGGGCGCTGCCAGGGCctTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
115	T10	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
116	SW2	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGcGTCCGGGTcCTGGAGGACGGCGTGAA
122	HK4	428 CCTTAGGGGGCGtTGCCAGaGCCCTGGCaCATGGtGTCCGGGTtTgTGGAGGACGGCGTGAA
109	SA10	428 CtTTAGGGGGCGCTGCCAGgGCCTTGGCGCATGGCGTCCGGGTtCTGGAAgACGGCGTGAA
110	S45	428 CCCTAGGGGGCGCTGCCAGaGCCTTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
123	P8	428 CCCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtTgTGGAGGACGGCGTGAA
124	T3	428 CctTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
120	HK3	428 CCCTAGGGGGCGTTGCCAGAGCCtTGGCACATGGTGTCCGGGTtCTGGAGGACGGCGTGAA
121	HK5	428 CCCTAGGGGGCGTTGCCAGAGCCcTGGCACAcGGTGTCCGGGTtCTGGAGGACGGCGTGAA
109-124 consensus		CccTAGGGGGcGcTGCCAGgGCcctTGGCGcATGGcGTCCGGGTtCTGGAgGACGGCGTGAA

SEQ ID NO:	ISOLATE	
119	S9	489 CTATGCAACAGGGAACcTcCCCCGGTTGCTCTTTCTCTATCTTCCTTcTgGCTTTGCTgTCC
117	IND3	489 CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTaGCTTTGCTATCC
118	IND8	489 CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTATCC
111	D1	489 tTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
112	US6	489 CTATGCAACAGGGAACtTGCCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
113	P10	489 CTATGCAACAGGGAATcTGCCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
114	DK1	489 CTAcGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTCTGtTGTCC
115	T10	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTCTGCTGTCC
116	SW2	489 CTATGCAACAGGGAATcTGCCCCGGTTGCTcCTTTCTATCTTCCTCTTGGCTtTGCTGTCC
122	HK4	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCCTTTCTATCTTCCTCTTGGCTtTGCTGTCC
109	SA10	489 CTATGCAACAGGGAATTTGCCCGGTTGCGcCTTTCTCTATCTTCCTCTTGGCTtTGCTGTCC
110	S45	489 CTATGCAACAGGGAATCTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTcTGCTGTCC
123	P8	489 CTATGCAACAGGGAATCTGCCTGGTTGCTCTTTCTCTATCTTCCTtTTGGCTTTGCTGTCTc
124	T3	489 tTAcGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
120	HK3	489 CTAtGCAACAGGGAATTaTACCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
121	HK5	489 CTAcGCAACAGGGAATaTACCCGGTTGCTCTTTCTCTATCTTCCTtTTGGCTTTGCTGTCC
109-124 consensus		cTAtGCAACAGGGAAttTgCCcGGTTGCTCtTtCTCTATCTTCCTcTgGCTtTGcTgTCC

SEQ ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCCAGCTTCCGCT
118	IND8	550 TGTTTGACCgTCCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCCAGCTTCCGCT
112	US6	550 TGTTTGACCATcCCAGCTTCCGCT

FIGURE 6B

113	P10	550	TGccTGACCATCCCAGCgTCCGCT
114	DK1	550	TGTtTGACCATCCCAGCTTCCGcc
115	T10	550	TGTCTGACCATCCCAGCTTCCGCT
116	SW2	550	TGTCTGACCATCCCAGCTTCCGCT
122	HK4	550	TGTTTGACCATCCCAGCTTCCGCT
109	SA10	550	TGTTTaACCATCCCAGCTTCCGCT
110	S45	550	TGcTTGACCATCCCAGCTTCCGCT
123	P8	550	TGtcTGACCATCCCAGCTTCCGCT
124	T3	550	TGCTTGACCATCCCAGCTTCCGCT
120	HK3	550	TGCTTGACCACCCAGCTTCCGCT
121	HK5	550	TGtcTGACCACCCAGtTCCGCT
109-124	consensus		TGttTgACCatcCCAGctTCCGct

09034691 052199B
069250" T6942060

FIGURE 6C

SEQ ID NO: ISOLATE

119	S9	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
117	IND3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
118	IND8	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
111	D1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
112	US6	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
113	P10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
114	DK1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
115	T10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
116	SW2	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
122	HK4	1	ATGAGCACGAATCCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGCCGCCACAGG
109	SA10	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
110	S45	1	ATGAGCACGAATCCTAAACCTCAAAGAAcAAACCAAACGTAACACCAACCGCCGCCACAGG
123	P8	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAAGcCGCCGCCACAGG
124	T3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
120	HK3	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
121	HK5	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCACAGG
108	DR4	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
104	US11	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
105	S14	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
106	SW1	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
107	S18	1	ATGAGCACaAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG
103	DK7	1	ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCACAGG

103-124 consensus

ATGAGCACgAaTCCTAAACCTCAAAGAAaAACCAAACGTAACACCAaCCGcCGCCACAGG

SEQ ID NO: ISOLATE

119	S9	62	ACGTtAAGTTCCCGGGCGGTGGtCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
117	IND3	62	ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
118	IND8	62	ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
111	D1	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
112	US6	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
113	P10	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
114	DK1	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
115	T10	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
116	SW2	62	ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
122	HK4	62	ACGTtAAGTTCCCGGGCGGTGGCCAGATCGTtGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109	SA10	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
110	S45	62	ACGTCAAGTTCCCGGGtGGcGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
123	P8	62	ACGTtAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
124	T3	62	ACGTtAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
120	HK3	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
121	HK5	62	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
108	DR4	62	ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTtGCCGCGCAGGGG
104	US11	62	ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTtGCCGCGCAGGGG
105	S14	62	ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTtGCCGCGCAGGGG
106	SW1	62	ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTtGCCGCGCAGGGG
107	S18	62	ACGTtAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTtGCCGCGCAGGGG
103	DK7	62	ACGTcAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTtGCCGCGCAGGGG

103-124 consensus

ACGTcAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTAcCTGTTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

119	S9	123	CCCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
117	IND3	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
118	IND8	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
111	D1	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
112	US6	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
113	P10	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
114	DK1	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
115	T10	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
116	SW2	123	CCCCcGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
122	HK4	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG

FIGURE 6C

109	SA10	123	CCCCAGGTTGGGTGTGCGCGCgAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
110	S45	123	CCCCAGGTTGGGTGTGCGCGCgACTAGGAAGACTTCCGAGCGGTcCaCAACCTCGTGGAAcGG
123	P8	123	CCCCAGGTTGGGTGTGCGCGCgACTAGGAAGACTTCCGAGCGaTCGCAACCTCGTGGcAGG
124	T3	123	CCCCAGGTTGGGTGTGCGCGCgACTAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
120	HK3	123	CCCCAGGTTGGGTGTGCGCGCgACCAGGAAGACTTcAGAGCGGTcGCAACCTCGTGGAAAGG
121	HK5	123	CCCCAGGTTGGGTGTGCGCGCgACCAGGAAGACTTCCGAGCGGTcGCAACCTCGTGGAAAGG
108	DR4	123	CCCTAGATTGGGTGTGCGCGCgACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
104	US11	123	CCCTAGATTGGGTGTGCGCGCgACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
105	S14	123	CCCTAGATTGGGTGTGCGCGCgACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
106	SW1	123	CCCTAGATTGGGTGTGCGCGCgACGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
107	S18	123	CCCTAGATTGGGTGTGCGCGCgACGAGGAAGACTTCCGAGCGGTcGCAACCTCGcGGTAGA
103	DK7	123	CCCTAGATTGGGTGTGCGCGCgCGAGGAAGACTTCCGAGCGGTcGCAACCTCGaGGTAGA

103-124 consensus

CCCcAGgTTGGGTGTGCGCGCgaCtAGGAAGACTTCCGAGCGgTCgCAACCTCGtGGAAgGg

SEQ ID NO: ISOLATE

119	S9	184	CGACAACCTATCCCCAAGGCTCGCCatCCCGAGGGcAGGGCCTGGGCTCAGCCCGGGTACC
117	IND3	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
118	IND8	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTAGGGCTCAGCCCGGGcACC
111	D1	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
112	US6	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
113	P10	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
114	DK1	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
115	T10	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
116	SW2	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
122	HK4	184	CGACAACCTATCCCCAAGGCTCGCCaCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
109	SA10	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
110	S45	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGCAtC
123	P8	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGCAtC
124	T3	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
120	HK3	184	CGACAACCTATCCCCAAGGCTCGCCaACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
121	HK5	184	CGACAACCTATCCCCAAGGCTCGCCGCGCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
108	DR4	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
104	US11	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
105	S14	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
106	SW1	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
107	S18	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103	DK7	184	CGTcAGCCTATCCCCAAGGCACGTcCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC

103-124 consensus

CGaCAaCCTATCCCCAAGGCTcCGcCgGcCCGAGGGcAGGgCCTGGGCTcCAGCCcGGGtAcc

SEQ ID NO: ISOLATE

119	S9	245	CTTGGCCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGtGG
117	IND3	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
118	IND8	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
111	D1	245	CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
112	US6	245	CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
113	P10	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
114	DK1	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
115	T10	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
116	SW2	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
122	HK4	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
109	SA10	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
110	S45	245	CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
123	P8	245	CTTGGCCCCCTCTATGGCaATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
124	T3	245	CTTGGCCCCCTCTATGGCaATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
120	HK3	245	CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
121	HK5	245	CTTGGCCCCCTCTATGGCAATGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
108	DR4	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
104	US11	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
105	S14	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
106	SW1	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG
107	S18	245	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTcACCCCCGCGG

245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG
CtTGGCCCCCTCTAtGgCaAtGAGGGCttgGGgTGGGCaGGATGGCTCCTGTCaCCCCgtGG

306 CTCTCGGCCTAGTTGGGGCCCCAatGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 CTCCCGGCCTAGTTGGGGCCCCACcGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
306 CTCCCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGcAATcTGGGTAAGGTC
306 CTCTCGGCCTAATTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
306 CTCTCGGCCTAGCTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
306 CTCcCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGcAAAGTC
306 CTCtCGGCCTAGCTGGGGCCCCaACAGACCCCCGGCGcAGGTCGCGCAATTTGGGcAAAGTC

CTCtCGGCCTAgTtTGGGGCCCCcAc-GACCCCCGGCGtAGGTCGCGtAATtTGGGtAAgGTC

367 ATCGATACCCTCACATGCGGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACgTGCGGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGgCC
367 ATCGATACCCTCACATGCGGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGctc
367 ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
367 ATCGAaACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
367 ATCGATACCCTtACGTGCGGCTTCGCCGACCTCATGGGGTACATACCgCTCGTCGGCGCCCC
367 ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATACCgCTCGTCGGCGCCCC
367 ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCCC
367 ATCGATACCCTtACGTGCGGCTTCGCCGACCTCATGGGGTACATaCCGCTCGTCGGCGCCCC

ATCGA⁺ACCCT⁻ACaTGCGGCTT⁻cGCCGACCTCATGGGGTACAT⁻tCCGCTCGTCGG⁻cGccc

428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA
428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA
428 CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA
428 CCCTAGGGGGTGCTGCCAGGGCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA
428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTGGAGGACGGCGTGAA

FIGURE 6C

113	P10	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
114	DK1	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
115	T10	428	CCCTAGGGGGCGCTGCCAGGGCtCTGGCaCATGGtGTCCGGGTTCTGGAGGACGGCGTGAA
116	SW2	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGcGTCCGGGTTcCTGGAGGACGGCGTGAA
122	HK4	428	CcTTAGGGGGCGtTGCCAGaGCCCTGGCaCATGGtGTCCGGGTTgTGGAGGACGGCGTGAA
109	SA10	428	CtTTAGGGGGCGCTGCCAGgGCCCTGGCGCATGGCGTCCGGGTTCTGGAAgACGGCGTGAA
110	S45	428	CCCTAGGGGGCGCTGCCAGaGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
123	P8	428	CCCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTgTGGAGGACGGCGTGAA
124	T3	428	CcTtAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
120	HK3	428	CCCTAGGGGGCGTTGCCAGAGCctTGGCACATGGTGTCCGGGTTCTGGAGGACGGCGTGAA
121	HK5	428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACaGGTGTCCGGGTTCTGGAGGACGGCGTGAA
108	DR4	428	CCCTtGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAAGACGGCGTGAA
104	US11	428	CtCTCGGaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
105	S14	428	CcCTCGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
106	SW1	428	CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
107	S18	428	CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA
103	DK7	428	CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAAGACGGCGTGAA

103-124 consensus CccTaGGgGGcGcTGCCAGgGCccTGGCGcCatGGcGTCCGgGTtctTGGAgGACGGCGTGAA

SEO ID NO:	ISOLATE	
119	S9	489 CTATGCAACAGGGAACcTcCCCCGGTTGCTCTTTCTCTATCTTCCTTcTgGCTTTGCTgTCC
117	IND3	489 CTATGCAACAGGGAACtTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTaGCTTTGCTATCC
118	IND8	489 CTATGCAACAGGGAACtTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTGCGCTTTGCTATCC
111	D1	489 tTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTTTGCTGTCC
112	US6	489 CTATGCAACAGGGAACtTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTTTGCTGTCC
113	P10	489 CTATGCAACAGGGAATcTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTTTGCTGTCC
114	DK1	489 CTAcGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTCTGtTGTC
115	T10	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTCTGtTGTC
116	SW2	489 CTATGCAACAGGGAATcTGCCCGGTTGCTCctTTTTCTATCTTCCTCTTGCGCTtTGCTGTCC
122	HK4	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTcTGCTGTCC
109	SA10	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTtTGCTGTCC
110	S45	489 CTATGCAACAGGGAATCTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTcTGCTGTCC
123	P8	489 CTATGCAACAGGGAATCTGCCTGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTcTGCTGTCC
124	T3	489 tTAcGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTTTGCTGTCC
120	HK3	489 CTAtGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTGCGCTTTGCTGTCC
121	HK5	489 CTAcGCAACAGGGAATaTACCCGGTTGCTCTTTCTCTATCTTCCTTTTGCGCTTTGCTGTCC
108	DR4	489 CTATGCAACAGGGAATCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGCGCTTTGCTGTCT
104	US11	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGCGCTTTGCTGTCT
105	S14	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTcCTaGCCCTGCTTTCT
106	SW1	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTTTCT
107	S18	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTCTCT
103	DK7	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTtTGGCCCTGCTCTCT

103-124 consensus cTAtGCAACAGGGAAtcTgCCcGGTTGCTCtTtCTCTATCTTCCTctTgGCTtTGcTgTCC

SEO ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCCAGCTTCCGCT
118	IND8	550 TGTTTGACCGtCCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCCAGCTTCCGCT
112	US6	550 TGTTTGACCATtCCAGCTTCCGCT
113	P10	550 TGccTGACCATCCCAGCGTCCGCT
114	DK1	550 TGTtTGACCATCCCAGCTTCCGc
115	T10	550 TGTCTGACCATCCCAGCTTCCGCT
116	SW2	550 TGTCTGACCATCCCAGCTTCCGCT
122	HK4	550 TGTTTGACCATCCCAGCTTCCGCT
109	SA10	550 TGTTTaACCATCCCAGCTTCCGCT
110	S45	550 TGcTTGACCATCCCAGCTTCCGCT
123	P8	550 TGtctGACCATCCCAGCTTCCGCT
124	T3	550 TGCTTGACCATCCCAGCTTCCGCT
120	HK3	550 TGCTTGACCAcCCcAGCTTCCGCT
121	HK5	550 TGtctGACCAcCCcAGtTTCCGCT

FIGURE 6C

108	DR4	550	TGctTGACCGTGCCCGCaTCgGCC
104	US11	550	TGCCTGACTGTGCCCGCTTCAGCC
105	S14	550	TGCCTGACTGTGCCCGCTTCAGCC
106	SW1	550	TGCCTGACaGTGCCCGCGTCAGCC
107	S18	550	TGtCTGACTGTGCCCGCGTCAGct
103	DK7	550	TGcCTGACcGTGCCCGCtTCgGCc
103-124	consensus		TGttTgACcatcCCaGctTCcGct

09084691 052693
369250" 16948060

FIGURE 6D

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	1 ATGAGCACAAATTCCTAAACCTCAAAGAAAAACCAAAGAAACACtAACCGTCGCCACAAg
125	T4	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACcAACCGTCGCCACAgG
126	US10	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACtAACCGTCGCCACAAg
127	T9	1 ATGAGCACAAATCCaAAACCcCAAAGAAAAACCAaAGAAACACcAACCGTCGCCACAgG
125-128	consensus	ATGAGCACAAATCCtAAACCTCAAAGAAAAACCAaAGAAACAC - AACCGTCGCCACAG - G
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGtTGCCGCGCAGGGG
125	T4	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCGCGCAGGGG
126	US10	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCGCGCAGGGG
127	T9	62 ACGTTAAGTTtCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCGCGCAGGGG
125-128	consensus	ACGTTAAGTT - CCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGtTGCCGCGCAGGGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	123 CCCcAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGgTCCcAGCCtCGTGGaAGG
125	T4	123 CCCcAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGaTCCcAGCCACGTGGGAGG
126	US10	123 CCCcAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGGTCCcAGCCACGTGGGAGG
127	T9	123 CCctAGGTTGGGTGTGCGCaGACAAGGAAGACTTCGGAGCGGTCCcAGCCACGTGGGAGG
125-128	consensus	CCCcAGGTTGGGTGTGCGCGcGACAAGGAAGACTTCGGAGCGgTCCcAGCCaCGTGGgAGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	184 CGCCAGCCCATCCCCtAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACcAGGATAcC
125	T4	184 CGCCAGCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACcAGGATAcC
126	US10	184 CGCCAGCCCATCCCCAAAGATCGGCGCcCCACTGGCAAGTCCTGGGGAAAACcAGGATAcC
127	T9	184 CGCCAGCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACcAGGATAcC
125-128	consensus	CGCCAGCCCATCCCCcAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACcAGGATAcC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	245 CCTGGCCCCCTGTATGGGAATGAGGGgCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
125	T4	245 CCTGGCCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
126	US10	245 CtTGGCCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
127	T9	245 CcTGGCCtCTATATGGGAATGAGGGACTCGGCTGGGCgGGATGGCTCCTGTCCCCCGAGG
125-128	consensus	CcTGGCCcCT - TATGGGAATGAGGGaCTCGGCTGGGCaGGATGGCTCCTGTCCCCCGAGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	306 TTCtCGTCCCTCtTGGGGCCCCAATGACCCCCGGCATAGGTCGCGCAAtGTGGGTAAaGTC
125	T4	306 TTCCCGTCCCTCtTGGGGCCCCAATGACCCCCGGCATAGGTCGCGCAACGTGGGTAAAGGTC
126	US10	306 TTCCCGTCCCTCTTGGGGCCCCAcTGAtCCCCGGCATAGGTCGCGCAACGTGGGTAAAGGTC
127	T9	306 TTCCCGTCCCTCTTGGGGCCCCAgTGAcCCCCGGCATAGGTCGCGCAACGTGGGTAAAGGTC
125-128	consensus	TTCcCGTCCCTCtTGGGGCCCCAaTGAcCCCCGGCATAGGTCGCGCAAcGTGGGTAAgGTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	367 ATCGATACCCTAACGTGCgGcTTGCCGACCTCATGGGTACaTCCCGTCGTAGGCGcCC
125	T4	367 ATCGATACCCTAACGTGCAGCcTTGCCGACCTCATGGGTACgTCCCGTCGTAGGCGgCC
126	US10	367 ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGaTACATCCCGTCGTgGGCGCtC
127	T9	367 ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGgTACATCCCGTCGTaGGCGCcC
125-128	consensus	ATCGATACCCTAACGTGCgGcTTGCCGACCTCATGGGgTACaTCCCGTCGTaGGCGccc
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	428 CGcTtGGTGGtGTCGCCAGAGCTCTtGCGCATGGCGTGAGAGTCCTGGAGGACGGaGTTAA

FIGURE 6D

125 T4
126 US10
127 T9

125-128 consensus

428 CGtTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA
428 CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgGTCCTGGAGGACGGGGTTAA
428 CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCAcGGCGTGAGaGTCCTGGAGGACGGGGTTAA

CGcTtGGTGGcGTcGCCAGAGCTCTcGCGCAtGGCGTGAGaGTCCTGGAGGACGGgGTTAA

SEQ ID NO: ISOLATE

128 T2
125 T4
126 US10
127 T9

125-128 consensus

489 TTATGCAACAGGtAACTTACCcGGTTGCTCCTTTTCTATcTTCTTGCTaGCCCTgCTGTCC
489 TTATGCAACAGGGAACtTACCtGGTTGCTCCTTTTCTATtTTCTTGCTGGCCCTACTGTCC
489 TTATGCAACAGGGAACtTACCcGGTTGCTCCTTTTCTATCTTCTTGCTGGCCtTACTGTCC
489 TTATGCAACAGGGAACcTACCtGGTTGCTCtTTTTCTATCTTCTTGCTGGCCcTACTGTCC

TTATGCAACAGGgAACTTACC-GGTTGCTCtTTTTCTATcTTCTTGCTgGCCcTaCTGTCC

SEQ ID NO: ISOLATE

128 T2
125 T4
126 US10
127 T9

125-128 consensus

550 TGCATCACtATTCCgGTtTCaGCT
550 TGCATCACCAttCCAGTCTCcGCT
550 TGCATCACCAttCCAGTCTCTGCT
550 TGCATCACCAcTCCgGcCTCTGCT

TGCATCACcAtTCC-GtcTCTcGCT

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869250" T6948060

FIGURE 6E

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1

129-133 consensus

1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG

ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCCGCCACAGG

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1

129-133 consensus

62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGTGGCGGGcAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG

ACGTtAAGTTCCCGGGTGGCGGGcAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1

129-133 consensus

123 CCCcAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGtCTTCCGAGCGATCCCAGCCGCGTGGGAGg
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA

CCCcAGGTTGGGTGTGCGCgCGACAAGGAAGaCTTCCGAGCGATCCCAGCCGCGTGGGAGa

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1

129-133 consensus

184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCCTGGGGAAAGCCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAGCCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAGCCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAGCCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAgCCAGGATATC

CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGtCCTGGGGAAAgCCaGGATATC

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1

129-133 consensus

245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245 CTTGGCCTCTtTACGGAAACGAGGGCTGCGGtTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245 CTTGGCCTCTgTACGGAAACGAGGGCTGCGGcTGGGCAGGTTGGCTCCTGTCCCCCGCGG

CTTGGCCcCTgTAtGGAAACGAGGGCTGCGGcTGGGCAGGTTGGCTCCTGTCCCCCGCGG

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1

129-133 consensus

306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAaATCACGCAATTTGGGtAAAGTC
306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAGTC
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAGTC
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGTAATTTGGGCAGgAGTC
306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCAcAGATCACGTAAcTTGGGCAagGTC

GTCTCgTCCTAcTTGGGGCCCCACTGACCCCCGGCAcAgATCACGCAAtTTGGGcAaaGTC

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8

367 ATCGACACCATTACGTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
367 ATCGACACCATTACGTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
367 ATCGACACCATTACGTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
367 ATCGATACCATTACaTGTGGTtTTGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC

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FIGURE 6E

130	US1	367	ATCGATACCATTACgTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC
129-133	consensus		ATCGAcACCATTACgTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC

SEQ ID NO:	ISOLATE		
131	DK11	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
132	SW3	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
133	DK8	428	CGGTtGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
129	T8	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGGGTCCTGGAAGACGGGATAAA
130	US1	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGGGTCCTGGAAGACGGGATAAA
129-133	consensus		CGGTcGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGgGTCCTGGAAGACGGGATAAA

SEQ ID NO:	ISOLATE		
131	DK11	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcCa
132	SW3	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcCG
133	DK8	489	TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcCG
129	T8	489	cTAtGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcCG
130	US1	489	tTAcGCAACAGGGAATcTGCCTGGTTGCTCtTTTTCTATCTTCTTaCTTGCTCTTCTGTcCg
129-133	consensus		tTAcGCAACAGGGAATcTGCCTGGTTGCTCtTTTTCTATCTTCTTaCTTGCTCTTCTGTcCg

SEQ ID NO:	ISOLATE		
131	DK11	550	TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550	TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550	TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550	TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550	TGCgcCACgGTGCCgGTGTCTGCA
129-133	consensus		TGct - CACaGTGCCaGTGTCTGcG

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FIGURE 6F

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8C
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACcAACCGTCGCCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACTAACCGTCGCCCACaG
1 ATGAGCACAAATCCaAAACCcCAAAGAAAAACCAaAGAAACACcAACCGTCGCCCACaGg
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACTAACCGTCGCCCACaG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACTAACCGcCGCCCACaGg

ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAaAGAAACACaAACCGcCGCCCACaGg

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
62 ACGTTAAGTTcCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
62 ACGTTAAGTTcCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
62 ACGTTAAGTTcCCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGCTGCCGCGCAGGGG
62 ACGTcAAGTTcCCGGGCGGtGGCCAGATCGTTGGCGGAGTATACTTGCTGCCGCGCAGGGG

ACGTTAAGTTcCCGGG-GGcGGcCAGATCGTTGGCGGAGT-TACTTGcTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

123 CCCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGAGtCTTCCGAGCGATCCCAGCCGCGTGGGAGg
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCACGTGGGAGG
123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGGTCCCAGCCACGTGGGAGG
123 CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGGTCCCAGCCcCGTGGaAGG
123 CCCgAGaTTGGGTGTGCGCGCGACgAGGAaACTTCCGaAGGTTCCCAGCCaCGTGGgAGG

CCCcAGgTTGGGTGTGCGCGCGACAAGGAAGaCTTCCGaAGCGaTCCCAGCCgCGTGGgAGg

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCCTGGGGAAAGCCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAAGCCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAaACCgGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGGAAaACCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTTGGGGAAaACCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCcCCACTGGCAAGTCTTGGGGAAaACCAGGATACC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTTGGGGAAaACCAGGATACC
184 CGCCAGCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTTGGGGAAaACCAGGATACC
184 CGCCAGCCCATCCCTAAAGATCGGCGCaCCACTGGCAAGTCTTGGGGAAgCCAGGATACC

CGCCAGCCCATCCCGAAAGATCGGCGCTCCAC-GGCAAGTCTTGGGGAAaCCaGGATATc

SEQ ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8

245 CTTGGCCCCCTGTATGGAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245 CTTGGCCCCCTGTATGGAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245 CTTGGCCCCCTGTATGGAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245 CTTGGCCTCTcTACGGAACGAGGGCTGCGGtTGGGCAGGTTGGCTCCTGTCCCCCGCGG

FIGURE 6F

130	US1	245	CTTGGCCTCTGTACGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
125	T4	245	CcTGGCCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
126	US10	245	CtTGGCCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
127	T9	245	CCTGGCCcCTATATGGGAATGAGGGACTCGGCTGGGCgGGATGGCTCCTGTCCCCCGAGG
128	T2	245	CCTGGCCCCCTGTATGGGAATGAGGGgCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
134	S83	245	CtTGGCCCCCTGTATGGGAATGAGGGcCTCGGCTGGGCAGGgTGGCTCCTGTCCCCCGcGG

125-134 consensus CcTGGCCcCTgTAtGG-AA-GAGGGc--CGGcTGGGCaGgTtTGGCTCCTGTCCCCCGcGG

SEQ ID NO: ISOLATE

131	DK11	306	GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAaATCACGCAATTTGGGtAAAGTC
132	SW3	306	GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAAGTC
133	DK8	306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAGTC
129	T8	306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGTAATTTGGGCAgAGTC
130	US1	306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCAcAGATCACGTAATTTGGGCAAGTC
125	T4	306	TTCCCGTCCCTCCTGGGGCCCCAaTGACCCCCGGCATAGGTTCGCGCAACGTGGGTAAGGTC
126	US10	306	TTCCCGTCCCTCTTGGGGCCCCAcTGATcCCCCGGCATAGGTTCGCGCAACGTGGGTAAGGTC
127	T9	306	TTCCCGTCCCTCTTGGGGCCCCAgTGACCCCCGGCATAGGTTCGCGCAACGTGGGTAAGGTC
128	T2	306	TTCTCGTCCCTCTTGGGGCCCCAaTGACCCCCGGCATAGGTTCGCGCAaGTGGGTAAaGTC
134	S83	306	TTCTCGcCCTTCaTGGGGCCCCAcGACCCCCGGCATAaATCGCGCAActTGGGTAAGGTC

125-134 consensus -TCtCgtCCt-ctTGGGGCCCCActGAcCCCCGGCAtAgaTC-CGcAA-tTGGGtAa-GTC

SEQ ID NO: ISOLATE

131	DK11	367	ATCGACACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC
132	SW3	367	ATCGACACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC
133	DK8	367	ATCGACACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC
129	T8	367	ATCGATACCATTACaTGtGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC
130	US1	367	ATCGATACCATTACGTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTCTGtGGCGCCC
125	T4	367	ATCGATACCCTAACGTGCaGcCTTGGCGACCTCATGGGGTACgTCCCCGTCTGtAGGCGgCC
126	US10	367	ATCGATACCCTAACGTGCGGCTTTGCGGACCTCATGGGaTACATCCCCGTCTGtGGCGcTc
127	T9	367	ATCGATACCCTAACGTGCGGCTTTGCGGACCTCATGGGGTACATCCCCGTCTGtAGGCGCCC
128	T2	367	ATCGATACCCTAACGTGCGGCTTTGCGGACCTCATGGGGTACATCCCCGTCTGtAGGCGCCC
134	S83	367	ATCGATACCCTAACGTGCGGtTTTGGCGACCTCATGGGGTACATaCCCCGTCTGtGGCGcTc

125-134 consensus ATCGAtACC-T-ACgTG-gGtTTTGGCGACCTCATGGGgTACaTcCC-GTCGTtGGCGcCC

SEQ ID NO: ISOLATE

131	DK11	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCCTGGAAGACGGGATAAA
132	SW3	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCCTGGAAGACGGGATAAA
133	DK8	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCCTGGAAGACGGGATAAA
129	T8	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACaTGGTGTAGAGTCCTGGAAGACGGGATAAA
130	US1	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTAGAGTCCTGGAAGACGGGATAAA
125	T4	428	CGtTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgTCTGAGGACGGGGTTAA
126	US10	428	CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCaCGGCGTGAGAGTCCTGAGGACGGGGTTAA
127	T9	428	CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCATGGCGTGAGgTCTGAGGACGGGGTTAA
128	T2	428	CGCTTGGTGGtGTcGCCAGAGCTCTcGCGCATGGCGTGAGAGTCCTGAGGACGGGaGTTAA
134	S83	428	CcgtTGGcGGcGTtGCCAGAGCcCTcGcCATGGgGTGAGgGTtCTGAGGACGGGaTaAA

125-134 consensus CggTtGGaGGcGTcGCCAGAGCTcTgGCaCA-GGtGT-AG-GTcCTGGA-GACGGGaTaAA

SEQ ID NO: ISOLATE

131	DK11	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTCa
132	SW3	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcG
133	DK8	489	TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcG
129	T8	489	cTAtGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTcCa
130	US1	489	TTAcGCAACAGGGAATcTGCTGGTTGCTCTTTTTCTATCTTCTTaCTTGCTCTTCTGTcGg
125	T4	489	TTATGCAACAGGGAACtTACCTGGTTGCTCTTTTTCTATCTTCTTCTTGCTGGCCtACTGTCC
126	US10	489	TTATGCAACAGGGAACtTACcGGTTGCTCTTTTTCTATCTTCTTCTTGCTGGCCtACTGTCC
127	T9	489	TTATGCAACAGGGAACcTACcTGGTTGCTCTTTTTCTATCTTCTTCTTGCTGGCCtACTGTCC
128	T2	489	TTATGCAACAGGtAACTTACCCGGTTGCTCctTTTTCTATCTTCTTCTTGCTaGCCCTgCTGTCC

FIGURE 6F

134	S83	489	TTATGCAACgGGgAAAtTTgCCCCGGTTGCTCtTTcTCTATCTTtcTctTgGCCCCtctTGTct
125-134	consensus		tTAtGCAACaGGgAAAttTgCCtGGTTGCTCtTTtTCTATcTTctTgcTtGC-cTtcTGTcc

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
131	DK11	550 TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550 TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550 TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550 TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550 TGCgcCACgGTGCCgGTGTCTGCA
125	T4	550 TGCATCACCATTCCAGTCTCcGCT
126	US10	550 TGCATCACCATTCCAGTCTCTGCT
127	T9	550 TGCATCACCacTCCGGcCTCTGCT
128	T2	550 TGCATCACTATTCCGGTTTCaGCT
134	S83	550 TGCATCtCTgTgCCaGTTTCcGCc
125-134	consensus	TGCatCaCagtgCCaGtgTCtGct

004591-0363
363350 "T6948050"

FIGURE 6G

SEQ ID NO: ISOLATE
 138 DK12
 135 HK10
 136 S52
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE
 138 DK12
 135 HK10
 136 S52
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE
 138 DK12
 135 HK10
 136 S52
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE
 138 DK12
 135 HK10
 136 S52
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE
 138 DK12
 135 HK10
 136 S52
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE
 138 DK12
 135 HK10
 136 S52
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE
 138 DK12
 135 HK10
 136 S52
 137 S2

135-138 consensus

SEQ ID NO: ISOLATE
 138 DK12

1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG
 1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG
 1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG
 1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG

ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCCACAGG

62 ACGTcAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
 62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
 62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
 62 ACaTcAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG

ACgT-AAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG

123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCaCAGCCTCGCGGACGg
 123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCgCAGCCTCGCGGACGA
 123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCACAGCCTCGCGGACGA
 123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCACAGCCTCGCGGACGg

CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCaCAGCCTCGCGGACG-

184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCtGGGTACC
 184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCCGGGTACC
 184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCCGGGTACC
 184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGaTCCTGGGCTCAGCCCGGGTACC

CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGgTCCTGGGCTCAGCCcGGGTACC

245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGgTGGCTCCTGTCCCCACGCGG
 245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGaTGGCTCCTGTCCCCACGCGG
 245 CTTGGCCCCCTCTATGGTAAtGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG
 245 CTTGGCCCCCTCTATGGTAAcGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG

CTTGGCCCCCTCTATGGTAAcGAGGGCTGCGGGTGGGCAGGgTGGCTCCTGTCCCCACGCGG

306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGgaGGTCCCGCAATTTGGGTAAgGTC
 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGa cGGTCCCGCAATTTGGGTAAAGTC
 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC
 306 CTCCCGTCCATCTTGGGGCCCAAAtGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC

CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGgaGGTCCCGCAATTTGGGTAAAGTC

367 ATCGATACCCTcACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
 367 ATCGATACCCTTACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
 367 ATCGATACCCTTACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
 367 ATCGATACCCTTACGTGCGGcTTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC

ATCGATACCCTcACGTGCGGaTTGCGCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC

428 CtGTAGGgGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA

FIGURE 6G

135 HK10
136 S52
137 S2

135-138 consensus

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA

CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA

489 TTTCGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCT
489 TTTCGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCT
489 TTTTGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCc
489 TTTTGCAACAGGGAACCTTGCCCGGTTGCTCtTTTTCTATCTTCCTTCTTGCCcTGTTCTCt

TTT-GCAACAGGGAACCTTGCCCGGTTGCTCcTTTTCTATCTTCCTTCTTGCTcTGTTCTCt

550 TGCcTAATTCATCCAGCAGCTAGT
550 TGCTTAATTCATCCAGCAGCTAGT
550 TGCTTAgtTTCATCCtGCAGCTAGT
550 TGCTTAaTTCATCCaGCAGCTAGT

TGCTTAaTTCATCCaGCAGCTAGT

09084591.052698

FIGURE 6H

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCcATGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCcATGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCcATGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCcATGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCcATGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCcATGG
1 ATGAGCACaATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGcCGCCcATGG

ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGcCGCCcATGG

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

62 ACGTTAAGTTCCCGGGTGGcGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG
62 ACGTTAAGTTCCCGGGCGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG
62 AtGTAAaTTCCCaGGCGGcGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG
62 AcGTAAaTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG
62 ATGTAAaTTCCCGGGTGGTGGtCAGATCGTTGGCGGAGTTTACTTGTGTCGCGCAGGGG
62 ATGTgAAATTCCCGGGcGGcGGcCAGATCGTTGGCGGAGTTTACTTGTgTGCCGCGCAGGGG

AcGT-AAgTTCCCGGGTGGtGGcCAGATCGTTGGCGGAGTTTACTTGTgTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

123 CCcTAGaTTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGGAGg
123 CCCAGgTTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGGAGA
123 CCCAGaTTGGGTGTGCGCaCaACTAGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGGAGA
123 CCCAGgTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTTCGCAACCTCGTGGCAGG
123 CCCAGgTTGGGTGTGCGCGGACTCGaAAGACTTCGGAGCGGTTCGCAACCTCGtGGCAGG
123 CCCAGgTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTTCGCAACCTCGcGGCAGG
123 CCCcGGTTGGGTGTGCGCGCagCTCGGAAGACTTCGGAGCGGTTCaCAACCTCGtGGCAGG

CCCcAggTTGGGTGTGCGCGcGgaCTcGgAAGACTTCGGAGCGGTTCgCAACCTCGtGGcAGg

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

184 CGCCAGCCTATCCCCAAGGCgCGcCaActcGAGGGtAGGTCTCTGGGCTCAGCCtGGGTATC
184 CGCCAGCCTATCCCCAAGGCACGTCTGAGGGAAGGTCTCTGGGCTCAGCCCGGTATC
184 CGTCAGCCTATCCCCAAGGCACGTCTGAGGGAAGGTCTCTGGGCTCaACCCGGGTACC
184 CGTCAGCCTATCCCCAAGGCACGTCTGAGGGAAGGTCTCTGGGCTCAGCCCGGTACC
184 CGTCaACCTATCCCCAAGGCgCGcCaGcCaGAGGGCAGaTCCTGGGCGCAGCCCGGTACC
184 CGTCAGCCTATCCCCcAGGCaCGtCGGTCCGAGGGCAGGTCTCTGGGCTCAGCCCGGTACC
184 CGTCAGCCTATCCCCaAGGCgCGcCGGTCCGAGGGCAGGTCTCTGGGCTCAGCCCGGTACC

CGtCAgCCTATCCCCaAGGCaCGtCggtccGAGGGcAGgTCCTGGGCTCaGCCCggGTACc

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

245 CtTGGCCcCTTTACGGcAATGAGGGcTGCGGGTGGGCGGGATGGCTCCTGTcACCCCGTGG
245 CATGGCCTCTTTACGGTAATGAGGGTTCGCGGTGGGCGGGATGGCTCCTGTcACCCCGTGG
245 CATGGCCTCTTTACGGTAATGAGGGTTCGCGGTGGGCGGGATGGCTCtTGTCACCCCGTGG
245 CATGGCCTCTTTACGGTAATGAaGGCTGtGGGTGGGcAGGtTGGCTCCTGTcCCCCGCGG
245 CTTGGCCcCTcTATGGCAATGAGGGCTGcGGGTGGGcAGGGTGGCTCCTGTcCTcCGCGG
245 CTTGGCCTCTTTATGGCAATGAGGGCTGTGGGTGGGcAGGGTGGCTCCTGTCCCCCGCGG
245 CTTGGCCcCTTTAcGGCAATGAGGGCTGTGGGTGGGcAGGGTGGCTCCTGTCCCCCGCGG

CtTGGCCTCTtTAcGGcAATGAGGGcTGcGGGTGGGcAGG-TGGCTCtTGTC-CCcCGcGG

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8

306 CTCTCGgCCGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAGGTC
306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAGGTC
306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAGGTC
306 CTCTCGACCGTCTTGGGGcCCAAATGATCCCCGGCGAGGTTCGCGCAATTGGGTAAGGTC

FIGURE 6H

139 Z4
142 Z5
141 Z1

139-145 consensus

306 CTCTCGGCCATCTTGGGGCCCAATGATCCCCGGCGGAGaTCGCGCAATCTGGGTAAGGTC
306 aTCTCGGCCATCTTGGGGCCaAAATGATCCCCGGCGTAGGTCCCGCAATCTGGGTAAGGTC
306 tTCcaGGCCgTCTTGGGGCCcAAATGATCCCCGGCGTAGGTCCCGtAAATCTGGGTAAaGTC

cTcTcGgCCgTCTTGGGGcCcaAAATGATCCCCGGCGgAGgTCcCGcAAAtTGGGTAAGGTC

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

367 ATCGATACcCTAACTTGGCGcTTCGCCGAcCTCATGGGATACATCCCGgTCGTAGGCGCCCC
367 ATCGATACtCTAACTTGGCGtTTCGCCGAtCTCATGGGATACATCCCGCTCGTAGGCGCCCC
367 ATCGATACCCTAACcTGCGGCTTtGCCGACCTCATGGGATACATCCCGCTCGTAGGCGCCCC
367 ATCGATACCCTcACGTGCGGCTTCGCCGACCTCATGGGATACATCCCGCTCGTGGGCGCCCC
367 ATCGATACCCTGACGTGCGGCTTCGCCGACCTCATGGGATACATCCCGaTCGTGGGCGCCCC
367 ATCGATACCCTGACGTGTGGCTTCGCCGACCTCATGGGATACATTCCGCTCGTcGGGCGCCCC
367 ATCGATACCCTGACGTGTGGCTTCGCCGACCTCATGGGATACATTCCGCTCGTaGGGCGCCCC

ATCGATACcCT-ACgTGcGGcTTCGCCGAcCTCATGGGATACATcCCGcTCGTaGGGCGCCCC

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

428 CCGTGGGtGGCGTCGCCAGaGCCCTGGCGCATGGcGTcAGGcTtTcTGGAGGACGGGgTCAA
428 CCGTGGGCGGCGTCGCCAGGGCCCTGGCaCATGGtGTTAGGGCTgTGGAGGACGGGATCAA
428 CCGTGGGCGGCGTCGCCAGGGCCCTaGCGCATGGCGTTAGGGCTcTGGAGGACGGGATtAA
428 CaGTaGGAAGGCGTCGCCAGaGCCCTGGCGCATGGCGTCAGGGCTGTGGAGGACGGGATcAA
428 CcGTgGGgGGCGTCGCCAGGGCtCTGGCGCATGGCGTCAGGGCTGTGGAGGACGGGATtAA
428 CaGTaGGTGGCGTCGCCAGGGCCtTGGCGCATGGCGTCAGGGCCcTGGAGGACGGAATcAA
428 CtGTgGGTGGCGTCGCCAGGGCCcTGGCGCATGGCGTCAGGGCCgTGGAGGACGGAATtAA

CcGTgGGtGGCGTCGCCAGgGCcTgGCgCATGGcGTcAGGgctgTGGAGGACGGgaTcAA

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

489 TTATGCAACAGGGAATCTTCCCGTTGCTCTTTCTCTATCTTCCTCTTGGCACTgCTcTCG
489 TTATGCAACAGGGAATCTTCCCGTTGCTCTTTCTCTATCTTCCTCTTGGCACTTCTTTTCG
489 TTATGCAACAGGGAACCTTCCCGTTGCTCTTTtTCTATCTTCCTCTTGGCACTTCTTTTCG
489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTCTTGGCACTTCTcTCG
489 CTATGCAACAGGGAATCTTCCcGGTTGCTCTTTCTCTATCTTCCTtTGGCACTTCTtTCG
489 CTATGCAACAGGGAATCTTCTGGTTGCTCtTTtTCTATCTTCCTaCTTGCACTTtTCTCG
489 CTAcGCAACAGGGAACCTTCCCTGGTTGCTCtTTcTCTATCTTtCTtCTTGCACTTtTCTCG

cTAtGCAACAGGGAAtCTTCCcGGTTGCTCtTTcTCTATCTTcCTcTgGCACTtTcTcTCG

SEQ ID NO: ISOLATE

145 DK13
143 Z6
144 Z7
140 Z8
139 Z4
142 Z5
141 Z1

139-145 consensus

550 TGCCTgACTGTTCCCGcTtTCGGCC
550 TGCCTaACTGTTCCCaCCTCGGCC
550 TGCCTgACTGTTCCCGCCTCGGCC
550 TGCCTaACcGTcCCAGCGTcTgCT
550 TGCCTcACTGTtCCAGCGTCgGCT
550 TGCTtTGACAACACCgGCATCcgCT
550 TGCtTGACAACACCgGCATCtGCC

TGCcTgACTgttCC-gC-TCgGCC

FIGURE 61

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCGCCGCCACAGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCGCCGCCACAGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCACAGG

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCGCCGCCACAGG

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTtTACTTGTGTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTGTGCCGCGCAGGGG

ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTtTACTTGTGTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

123 CCCTaGgtTGGGTGTGCGCGGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
123 CCCTeGtaTGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGaCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
123 CCCTAGaTTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
123 CCCTAGgTTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
123 CCCAGGTTGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGGCGG
123 CCCAGGTTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
123 CCCtAGGTTGGGTGTGCGCGCaACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG

CCCTaGgtTGGGTGTGCGCGGgACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

184 CGTCAGCCTATTCCCAAGGCGCGCAaCCaCGGGcCGGTCTGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAAtCCgCGGGtCGGTCTGGGGTCAACCCGGGTACC
184 CGCCAGCCTATTCCCAAGGCGCGCAACCCACGGGCCGGTCTGGGGTCAACCCGGGTACC
184 CGCCAGCCTATTCCCAAGGCGCGCAACCCACGGGCCGGTCTGGGGTCAACCCGGGTACC
184 CGCCAGCCTATTCCCAAGGCGCGCAACCCACGGGCCGGTCTGGGGTCAACCCGGGTACC
184 CGCCAGCCTATTCCCAAGGcCGCCAGCCCACGGGCCGGTCTGGGGTCAACCCGGGTACC
184 CGtCAGCCTATtCCCAAGGcCGCCAGCCCACGGGCCGGTCTGGGGTCAACCCGGGTACC

CGcCAGCCTATtCCCAAGGcCGCCaCCaCGGGcCGGTCTGGGGTCAACCCGGGTACC

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

245 CTTGGCCCCtTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGtTGCTCTCCCCcCGAGG
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCGAGG
245 CTTGGCCCCTTTACGCCAATGAGGGCCTCGgGTGGGCAGGGTGGTTGCTCTCCCCCGAGG
245 CTTGGCCCCTTTAtGCCAATGAGGGCCTCGgGTGGGCAGGGTGGTTGCTCTCCCCCGAGG
245 CTTGGCCCCTTTAtGCCAATGAGGGCCTCGgGTGGGCAGGGTGGTTGCTCTCCCCCGAGG

CTTGGCCCCtTTTAcGCCAATGAGGGCCTCGgGTGGGCAGGGTGGtTGCTCTCCCCcCGAGG

FIGURE 6I

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

306 CTCTCGGCCTAAcTGGGGCCCCAATGACCCCCGGCGAAgATCGCGCAATTTGGGcAAGGTC
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
306 CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC

CTCTCGGCCTAatTGGGGCCCCAatGACCCCCGGCGaAaaTCGCGCAatTTGGGtAAGGTC

367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC

ATCGAtACCCTaACgTGCGGATTGCGCGAcCTCATGGGGTACATCCCGCTCGTAGGCGGCC

428 CCGTTGGGGGCGTCGCAAGGGCcCTCGCACACGGTGTGAGaGcCTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCcCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCCTtGCACATGGTGTGAGGGTCTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCCTCGCACATGGTGTGAGGGTCTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCTCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCTCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAA

CCGTTGGGGGCGTCGCAAGGGCcCTcGCACAcGGTGTGAGgGtCTTGAGGACGGGGTAAA

489 tTATGCAACAGGGAATcTtCCCCGGTTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTgTCCTTGCACTTCTCTCG
489 CTATGCAACgGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 tTACGCAACAGGGAATcTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 CTACGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTTc
489 CTACGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
489 CTAtGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA

cTAtGCAACaGGAATtTgCCCCGGTTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTcTCg

550 TGcTgACCGTCCCgGCCaCTGCA
550 TGCCTaACCGTCCCtGCCTCTGCA
550 TGCCTGACCGTCCCgGCCTCTGCA
550 TGcTgACCGTCCCAGCCTCTGCA
550 TGCCTGACCGTCCCAGCCTcGCA
550 TGtCTGAtCaTCCCGGCCTCTGCA
550 TGCCTGACCGTCCCgGCCTCTGCA
550 TGCCTGACTGTCCCGaCCTCTGcC

TGccTgAccgTCCCgGCtCtGCa

FIGURE 6J

SEQ ID NO:	Genotype		
103-154	cons.	1	ATGAGCACgaaTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcACcAaCCgcCGCCcAcagG
103-124	1	1	ATGAGCACgAaTCCTAAACCTCAAAGAAaAaACCaaACGTAACACCAaCCgcCGCCcACAGG
125-134	2	1	ATGAGCACAAaTCCTAAACCTCAAAGAAAAACCAaAGAAAcACaAACCGcCGCCcACagG
135-138	3	1	ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAAGAAACACCATCCGTCGCCcACAGG
139-145	4	1	ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGcCGCCcATGG
146-153	5	1	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAaAGAAACACCAACCGcCGCCcACAGG
154	6	1	ATGAGCACACTTCCAAaACCCCAAAGAAAAACCAAAAGAAACACCAACCGTCGCCcAACGG
SEQ ID NO:	Genotype		
103-154	cons.	62	AcgTcAAgTTcCCgGGcGGtGGtCAGATCGTtGGtGGAGTtTAcTtGtTGCCCGCGCAGGGG
103-124	1	62	ACGTcAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTAcTtGtTGCCCGCGCAGGGG
125-134	2	62	ACGTtAAGTTcCCGGGcGGcGGcCAGATCGTtGGCGGAGTtTAcTtGtTGCCCGCGCAGGGG
135-138	3	62	ACgTcAAGTTCCCGGGTGGCGGACAGATCGTtGGTGGAGTtTAcTtGtTGCCCGCGCAGGGG
139-145	4	62	AcGTaAAGTTCCCGGGcGGtGGtGGcCAGATCGTtGGCGGAGTtTAcTtGtTGCCCGCGCAGGGG
146-153	5	62	ACGTcAAGTTCCCGGGcGGTGGTcAGATCGTtGGTGGAGTtTAcTtGtTGCCCGCGCAGGGG
154	6	62	ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTtGGCGGAGTtTAcTtGtTGCCCGCGCAGGGG
SEQ ID NO:	Genotype		
103-154	cons.	123	CCCcaGgtTGGGTGTGCGCGcGgaCtaGgAAgaCTTCcGAgCGgTCgCAaCCtcGtGGaaGg
103-124	1	123	CCCcaGgtTGGGTGTGCGCGCGgaCtaAGGAAGACTTCcGAGCGgTCgCAACCTCGtGGaaGg
125-134	2	123	CCCcAGgtTGGGTGTGCGCGcCGACaAGGAAGaCTTCcGAgCGaTCCAGCCgCGTGGgAGg
135-138	3	123	CCCACGATTGGGTGTGCGCGCGACCGCTAAaACTTCGTAACGGTCaCAGCCTCGCGGACGa
139-145	4	123	CCCcaGgtTGGGTGTGCGCGcGgaCTcGgAAGACTTCGAGCGGTcGCAACCTCGtGGcAGg
146-153	5	123	CCCTaGgtTGGGTGTGCGCGCGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
154	6	123	CCCCCGGTGGGTGTGCGCGCGACGAGAAAGACTTCGAGCGATCCAGCCcAGAGGCAGG
SEQ ID NO:	Genotype		
103-154	cons.	184	CGaCAGCCtATcCCcaAgGctCGcCggccccgagGGcaggtcCTGGGctcagCCcGGgtAcC
103-124	1	184	CGaCAaCCtATCCCCAAGGctCGcCggCCCCGAGGGcAGGgCCTGGGctCAGCCcGGgtAcC
125-134	2	184	CGCCAGCCCATCCCCgAAAGATCGGCGctCCAcTGGCAAGtCCTGGGGAAaCCaGGATAtC
135-138	3	184	CGACAGCCTATCCCCAAGGCGCGTCGGAGCGGAAGGCCGgTCTGGGCTCAGCCcGGGTACC
139-145	4	184	CGtCAGCCTATCCCCaAGGCaCGtCggtccGAGGGcAGgTCTGGGCTCAGCCcGGGTACC
146-153	5	184	CGcCAGCCTATcCCCAAGGCGCGCCaAcCCaCGGgcCGGTCTGGGGTCAACCCGGGTACC
154	6	184	CGCCAACCTATACCAaAGGCGCGCCAGCCCCAGGGCAGGCACTGGGCTCAGCCCGGATACC
SEQ ID NO:	Genotype		
103-154	cons.	245	CtTGGCCcCtTcTAtGgcaAtGAGGGcttcGggTGGGCaGGaTGGcTccTgTCcCCcCgcGG
103-124	1	245	CtTGGCCCCCTCTAtGgCaAtGAGGGcttgGGgTGGGCaGGATGGCTCCTGTcACCCCGtGG
125-134	2	245	CtTGGCCcCtGtTAtGGgAAAtGAGGGcctCGGcTGGGCaGGtTGGCTCCTGTCCCCCGcGG
135-138	3	245	CTTGGCCCCCTCTATGGTAaAGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
139-145	4	245	CtTGGCCcCtTcTAcGGcAAAtGAGGGcTgCGGGTGGGCaGGgTGGCTCctGTcCCcCGcGG
146-153	5	245	CTTGGCCCCcTTTAcGCCAATGAGGGCCTCGgTGGGcAGGGTGGtTGCTCTCCCCcCGAGG
154	6	245	CTTGGCCTCTTTATGGAACGAGGGCTGTGGGTGGGcAGGtTGGCTCCTGTCCCCCGCGG
SEQ ID NO:	Genotype		
103-153	cons.	306	cTCtcggCCtagtTGGGGcCccActGAcCCCCGGCgtaggTCgCGcAAAtTGGGtAagGTC
103-124	1	306	cTCtcCGGCCTAgTGGGGCCCCcAcaGACCCCCGGCGtAGGTTCGCGtAAAtTGGGtAAGGTC
125-134	2	306	tTCtCgtCCtctTGGGGCCCCActGAcCCCCGGCAtAgaTCgCGcAAAtTGGGtAagGTC
135-138	3	306	CTCCCGTCCATCTTGGGGCCCCAAAcGACCCCCGGCGgaGGTCCCGCAATTTGGGTAAAGTC
139-145	4	306	cTCtcGgCCgTCTTGGGGcCcaAATGATCCCCGGCGgAGgTCcCGcAAAtTGGGTAAAGTC
146-153	5	306	CTCTCGGCCTAAtTGGGGCCCCAAtGACCCCCGGCGaAaaTCGCGCAAtTGGGTAAAGGTC
154	6	306	CTCCCGGCCACATTGGGGCCCCAATGACCCCCGGCGTCGATCCCGGAATTTGGGTAAAGGTC

FIGURE 6J

SEQ ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

367 ATCGAtACcctACgTGcgGctTcGCCGAcCTCATGGGgTACaTcCCGcTCGTcGGcGccc
367 ATCGAtACCCTcACaTGCGGCTTcGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc
367 ATCGAtACCcTaACgTGcgGttTTGCCGACCTCATGGGgTACaTcCCcGTCTGTtGGCGccc
367 ATCGATACCCTtACGTGCGGaTTCCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
367 ATCGATACcCTgACgTGcGGcTTcGCCGAcCTCATGGGATACATcCCGcTCGTaGGCGCCC
367 ATCGAtACCCTaACgTGCGGATTTCGCCGAcCTCATGGGGTACATCCCGCTCGTAGGCGGCC
367 ATCGATACCCTAACGTGTGGGTTTCGCCGATCTCATGGGGTACATtCCCGTCGTGGGCGCGC

SEQ ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

428 CcgTaGGgGGcGtcGcCaggGCcctTgGCgCatGGcGTcaGggttcTgGAgGACGGgTgAA
428 CccTaGGgGGcGcTGCCAGgGCcctTGGCgCatGGcGTCCGgGTtctTGGAgGACGGCGTGAA
428 CggTtGGaGGcGTcGCCAGAGCtCTgGCaCatGGtGTgAGgGTcCTGGAGGACGGGaTaAA
428 CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTGAAGACGGGATAAA
428 CcGTgGGtGGCGTCGCCAGgGCcctTgGCgCATGGcGTcAGGgctgTGGAGGACGGGaTcAA
428 CCGTTGGGGGCGTCGCAAGGGCtCTcGCACAcGGTGTGAGgGttCTTGAGGACGGGGTAAA
428 CTTTGGGCGGCGTCGCGCTCGCCTCGCACATGGCGTGAGGGCAATCGAGGACGGGATCAA

SEQ ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

489 cTatGCAACaGGgAAAttTgCCcGGTTGCTCtTTcTCTATcTTccTccTgGCTcTgcTgTCC
489 cTAtGCAACAGGGAAtcTgCCcGGTTGCTCtTTcTCTATCTTCCtctTgGCTtTgcTgTCC
489 tTAtGCAACaGGgAAAttTgCCcGGTTGCTCtTTtTCTATcTTctTgcTtGCccTtcTGTCc
489 TTTcGCAACAGGGAACTTGCCCCGGTTGCTCtTTTTCTATCTTCCtTCTTGCTcTGTTCTCt
489 cTAtGCAACAGGGAAcTTCCcGGTTGCTCtTTcTCTATCTTcCTctTgGCACTtctTcTCG
489 cTAtGCAACaGGGAATtTgCCCCGGTTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTcTCg
489 TTATGCAACAGGGAACTCCCCGGTTGCTCTTTCTCTATCTTCCtTTTGGCACTACTCTCG

SEQ ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

550 TGcctgaccgtcCCagcttCtgct
550 TGttTgACcatcCCaGctTCcGCT
550 TGCatCaCagtGCCaGtgTCTGCT
550 TGCTTAaTTCATCCaGCAGCTAGT
550 TGcCTgACTgttCCagCgTCgGCC
550 TGccTgAccgTCCCgGCCtCtGCa
550 TGCCTCACAACGCCAGCTTCGGCT

09084691 052698
869250 "T6948060

[illegible]

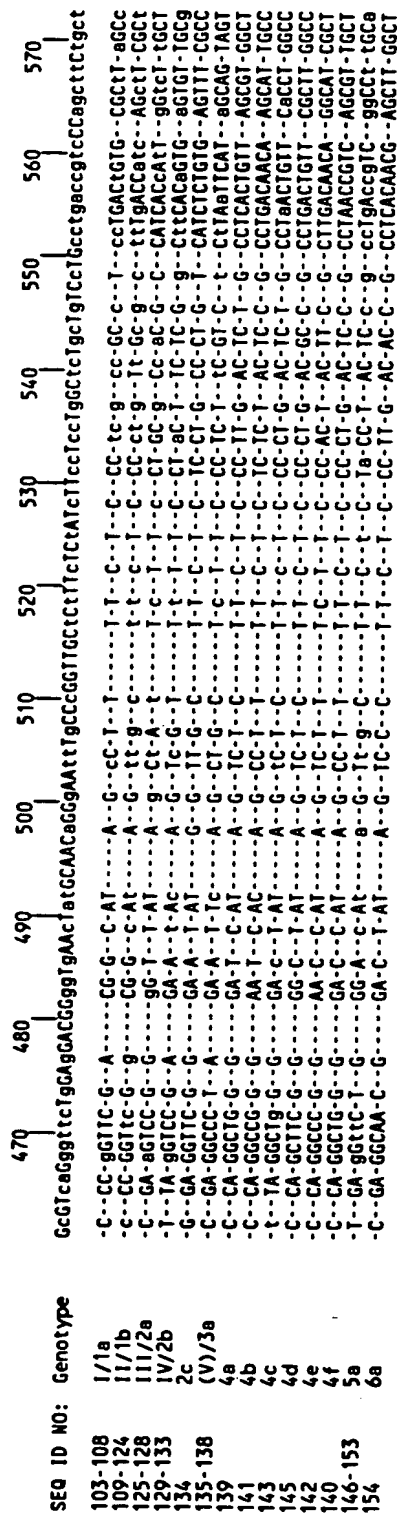


FIGURE 7A

SEO ID NO: ISOLATE
 156 US11
 157 S14
 158 SW1
 159 S18
 160 DR4
 155 DK7

155-160 consensus

1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

SEO ID NO: ISOLATE
 156 US11
 157 S14
 158 SW1
 159 S18
 160 DR4
 155 DK7

155-160 consensus

62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
 62 RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV

RQIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV

SEO ID NO: ISOLATE
 156 US11
 157 S14
 158 SW1
 159 S18
 160 DR4
 155 DK7

155-160 consensus

123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

SEO ID NO: ISOLATE
 156 US11
 157 S14
 158 SW1
 159 S18
 160 DR4
 155 DK7

155-160 consensus

184 CLTVPASA
 184 CLTVPASA
 184 CLTVPASA
 184 CLTVPASA
 184 CLTVPASA
 184 CLTVPASA

CLTVPASA

0908451.052593

06084691 06084690 06084689 06084688 06084687 06084686 06084685 06084684 06084683 06084682 06084681 06084680 06084679 06084678 06084677 06084676 06084675 06084674 06084673 06084672 06084671 06084670 06084669 06084668 06084667 06084666 06084665 06084664 06084663 06084662 06084661 06084660 06084659 06084658 06084657 06084656 06084655 06084654 06084653 06084652 06084651 06084650 06084649 06084648 06084647 06084646 06084645 06084644 06084643 06084642 06084641 06084640 06084639 06084638 06084637 06084636 06084635 06084634 06084633 06084632 06084631 06084630 06084629 06084628 06084627 06084626 06084625 06084624 06084623 06084622 06084621 06084620 06084619 06084618 06084617 06084616 06084615 06084614 06084613 06084612 06084611 06084610 06084609 06084608 06084607 06084606 06084605 06084604 06084603 06084602 06084601 06084600 06084599 06084598 06084597 06084596 06084595 06084594 06084593 06084592 06084591 06084590 06084589 06084588 06084587 06084586 06084585 06084584 06084583 06084582 06084581 06084580 06084579 06084578 06084577 06084576 06084575 06084574 06084573 06084572 06084571 06084570 06084569 06084568 06084567 06084566 06084565 06084564 06084563 06084562 06084561 06084560 06084559 06084558 06084557 06084556 06084555 06084554 06084553 06084552 06084551 06084550 06084549 06084548 06084547 06084546 06084545 06084544 06084543 06084542 06084541 06084540 06084539 06084538 06084537 06084536 06084535 06084534 06084533 06084532 06084531 06084530 06084529 06084528 06084527 06084526 06084525 06084524 06084523 06084522 06084521 06084520 06084519 06084518 06084517 06084516 06084515 06084514 06084513 06084512 06084511 06084510 06084509 06084508 06084507 06084506 06084505 06084504 06084503 06084502 06084501 06084500 06084499 06084498 06084497 06084496 06084495 06084494 06084493 06084492 06084491 06084490 06084489 06084488 06084487 06084486 06084485 06084484 06084483 06084482 06084481 06084480 06084479 06084478 06084477 06084476 06084475 06084474 06084473 06084472 06084471 06084470 06084469 06084468 06084467 06084466 06084465 06084464 06084463 06084462 06084461 06084460 06084459 06084458 06084457 06084456 06084455 06084454 06084453 06084452 06084451 06084450 06084449 06084448 06084447 06084446 06084445 06084444 06084443 06084442 06084441 06084440 06084439 06084438 06084437 06084436 06084435 06084434 06084433 06084432 06084431 06084430 06084429 06084428 06084427 06084426 06084425 06084424 06084423 06084422 06084421 06084420 06084419 06084418 06084417 06084416 06084415 06084414 06084413 06084412 06084411 06084410 06084409 06084408 06084407 06084406 06084405 06084404 06084403 06084402 06084401 06084400 06084399 06084398 06084397 06084396 06084395 06084394 06084393 06084392 06084391 06084390 06084389 06084388 06084387 06084386 06084385 06084384 06084383 06084382 06084381 06084380 06084379 06084378 06084377 06084376 06084375 06084374 06084373 06084372 06084371 06084370 06084369 06084368 06084367 06084366 06084365 06084364 06084363 06084362 06084361 06084360 06084359 06084358 06084357 06084356 06084355 06084354 06084353 06084352 06084351 06084350 06084349 06084348 06084347 06084346 06084345 06084344 06084343 06084342 06084341 06084340 06084339 06084338 06084337 06084336 06084335 06084334 06084333 06084332 06084331 06084330 06084329 06084328 06084327 06084326 06084325 06084324 06084323 06084322 06084321 06084320 06084319 06084318 06084317 06084316 06084315 06084314 06084313 06084312 06084311 06084310 06084309 06084308 06084307 06084306 06084305 06084304 06084303 06084302 06084301 06084300 06084299 06084298 06084297 06084296 06084295 06084294 06084293 06084292 06084291 06084290 06084289 06084288 06084287 06084286 06084285 06084284 06084283 06084282 06084281 06084280 06084279 06084278 06084277 06084276 06084275 06084274 06084273 06084272 06084271 06084270 06084269 06084268 06084267 06084266 06084265 06084264 06084263 06084262 06084261 06084260 06084259 06084258 06084257 06084256 06084255 06084254 06084253 06084252 06084251 06084250 06084249 06084248 06084247 06084246 06084245 06084244 06084243 06084242 06084241 06084240 06084239 06084238 06084237 0

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
175	P8
170	IND8
162	S45
171	S9
163	D1
165	P10
169	IND3
164	US6
166	DK1
167	T10
168	SW2
161	SA10
174	HK4
172	HK3
176	T3
173	HK5

[illegible]

161-176 consensus

MSTnPKPQRkTKRNTnRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR

<u>SEQ</u>	<u>ID NO:</u>	<u>ISOLATE</u>
175		P8
170		IND8
162		S45
171		S9
163		D1
165		P10
169		IND3
164		US6
166		DK1
167		T10
168		SW2
161		SA10
174		HK4
172		HK3
176		T3
173		HK5

62 RQIPKARRPEGRAWAQPGHPWPLYaNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGHPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGHPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARhPEGRAWAQPGPYWPPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGPYWPPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGPYWPPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGPYWPPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGPYWPPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGPYWPPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRAWAQPGPYWPPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRAWAQPGPYWPPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRAWAQPGPYWPPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRtWAQPGPYWPPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRtWAQPGPYWPPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARQPEGRtWAQPGPYWPPLYGNEGMGWAGWLLSPRGSRENWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGPYWPPLYGdEGMGWAGWLLSPRGSRPnWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRcWAQPGPYWPPLYGnEGMGWAGWLLSPhGSRPsgWGPTDPRRRSRNLGKV

161-176 consensus

RQPIPKARrPEGRaWAQPgYPWPLYgnEG-GWAGWLLSPrGSRPsWGpTDPRRRSRNLGKV

<u>SEO ID NO:</u>	<u>ISOLATE</u>
175	P8
170	IND8
162	S45
171	S9
163	D1
165	P10
169	IND3
164	US6
166	DK1
167	T10
168	SW2
161	SA10
174	HK4
172	HK3
176	T3
173	HK5

[illegible]

161-176 consensus

IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVIEDGVNYATGNIPGcSFSIFLLALLS

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
175	P8
170	IND8
162	S45

184 CLTiPASA
184 CLTvPASA
184 CLTiPASA

FIGURE 7B

171	S9	184	CLTIPASA
163	D1	184	CLTIPASA
165	P10	184	CLTIPASA
169	IND3	184	CLTIPASA
164	US6	184	CLTIPASA
166	DK1	184	CLTIPASA
167	T10	184	CLTIPASA
168	SW2	184	CLTIPASA
161	SA10	184	CLTIPASA
174	HK4	184	CLTIPASA
172	HK3	184	CLTtPASA
176	T3	184	CLTiPASA
173	HK5	184	CLTtPvSA
161-176	consensus		CLTiPaSA

09034591.052698

[illegible][illegible]

MSTnPKPQRkTKRNTnRRPQDVKFPGGGOIVGGVYLLPRRGPRLGVRAtBKTSEERSOPRGR

62 RQIPKARRPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPhGSRPswGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGdEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
62 RQIPKAROEGRtWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
62 RQIPKAROEGRtWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKAROEGRtWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKAROEGRAWAQPYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKAROEGRAWAQPYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGHPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARRPEGRaWAQPGHPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARhPEGRaWAQPGYPWPLYGnEGlGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
62 RQIPKARtPEGRaWAQPGHPWPLYaNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV

RQPIPKARrPEGRaWAQPGyPWPLYgnEG-GWAGWLLSPrGSRPsWGPTtDPRRRSRNLGKV

[illegible]

FIGURE 7C

159	S18	123	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
160	DR4	123	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
155	DK7	123	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
170	IND8	123	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
162	S45	123	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
171	S9	123	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
175	P8	123	IDTLTCGFADLMGYIPLVGgPLGGvARALAHGVRVvEDGVNYATGNLPGCSFSIFLLALLS

155-176	consensus	IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVlEDGVNYATGNlPGCsFSIFLLALLS
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<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
173	HK5	184 CLTtPvSA
176	T3	184 CLTiPASA
172	HK3	184 CLTtPASA
174	HK4	184 CLTiPASA
161	SA10	184 CLTiPASA
168	SW2	184 CLTiPASA
167	T10	184 CLTiPASA
166	DK1	184 CLTiPASA
164	US6	184 CLTiPASA
169	IND3	184 CLTiPASA
165	P10	184 CLTiPASA
163	D1	184 CLTiPASA
156	US11	184 CLTVPASA
157	S14	184 CLTVPASA
158	SW1	184 CLTVPASA
159	S18	184 CLTVPASA
160	DR4	184 CLTVPASA
155	DK7	184 CLTVPASA
170	IND8	184 CLTVPASA
162	S45	184 CLTiPASA
171	S9	184 CLTiPASA
175	P8	184 CLTiPASA

155-176	consensus	CLTiPaSA
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09084691.052698

FIGURE 7D

SEQ ID NO: ISOLATE
179 T9
178 US10
180 T2
177 T4

177-180 consensus

SEQ ID NO: ISOLATE
179 T9
178 US10
180 T2
177 T4

177-180 consensus

SEQ ID NO: ISOLATE
179 T9
178 US10
180 T2
177 T4

177-180 consensus

SEQ ID NO: ISOLATE
179 T9
178 US10
180 T2
177 T4

177-180 consensus

1 MSTNPKPQRKtiRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTiPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR

62 RQIPKDRRsTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPsdPRHRSRNVGKV
62 RQIPKDRRpTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPtDPRHRSRNVGKV
62 RQIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
62 RQIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
RQIPKDRRsTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRHRSRNVGKV

123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCslADLMGYvPVVGgPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
IDTLTCgfADLMGYiPVVGaPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

184 CITtPaSA
184 CITIPVSA
184 CITIPVSA
184 CITIPVSA

CITiPvSA

0004691.05299
869250" T 6948660

FIGURE 7E

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8

181-185 consensus

1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSESRQPRGR

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8

181-185 consensus

62 RQPIPKDRRSTGKpWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
62 RQPIPKDRRSTGKSWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV
62 RQPIPKDRRSTGKSWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGrV
62 RQPIPKDRRSTGKSWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
62 RQPIPKDRRSTGKSWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV

RQPIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGsrPtWGPTDPRHrSRNLGkV

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8

181-185 consensus

123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS

IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8

181-185 consensus

184 CcTVPVSA
184 CFTVPVSA
184 CFTVPVSA
184 CaTVPVSA
184 CcTVPVSA

C-TVPVSA

FIGURE 7F

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR

MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSESRQPRGR

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

62 RQIPKDRRSTGKpWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHrSRNLGKV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGrV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
62 RQIPKDRRtTGKsWGpPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHkSRNLGKV
62 RQIPKDRRpTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNLGKV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNLGKV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNLGKV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNLGKV
62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRHrSRNLGKV

RQIPKDRRsTGKsWGkPGYPWPLYGNEG-GWAGWLLSPRGsRpSwGPTDPRHrSRNLGkv

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCsLADLMGYvPVVGgPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

IDT-TCGfADLMGYiPVVGaPvGGVARALAHGVRVLEDGiNYATGNLPGCSFSIFLLALLS

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

184 CcTVPVSA
184 CFTVPVSA
184 CFTVPVSA
184 CaTVPVSA
184 CcTVPVSA
184 CIsVPVSA
184 CITIPVSA
184 CITIPVSA
184 CITtPaSA
184 CITiPvSA

CitvPvSA

FIGURE 7G

SEQ ID NO: ISOLATE
189 S2
187 HK10
190 DK12
188 S52

187-190 consensus

SEQ ID NO: ISOLATE
189 S2
187 HK10
190 DK12
188 S52

187-190 consensus

SEQ ID NO: ISOLATE
189 S2
187 HK10
190 DK12
188 S52

187-190 consensus

SEQ ID NO: ISOLATE
189 S2
187 HK10
190 DK12
188 S52

187-190 consensus

1 MSTLPPKPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR
1 MSTLPPKPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR
1 MSTLPPKPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR
1 MSTLPPKPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR
MSTLPPKPKQKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSESRQPRGR

62 RQPIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
62 RQPIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
62 RQPIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
62 RQPIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
RQPIPKARRSEGRSWAQPYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV

123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS

184 CLHHPAAS
184 CLHHPAAS
184 CLHHPAAS
184 CLVHPAAS

CLHHPAAS

09084691.052698

FIGURE 7H

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13

191-197 consensus

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13

191-197 consensus

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13

191-197 consensus

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13

191-197 consensus

1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRaARKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
 1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRatRKTSERSQPRGR

62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGqNDPRRRSRNLGKV
 62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
 62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
 62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
 62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
 62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
 62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
 62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV

RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGpNDPRRRSRNLGKV

123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRaledGINYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRaledGINYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRaledGINYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRaledGINYATGNLPGCSFSIFLLALLS
 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRaledGINYATGNLPGCSFSIFLLALLS

IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS

184 CLTTPASA
 184 CLTTPASA
 184 CLTVPASA
 184 CLTVPtSA
 184 CLTVPASA
 184 CLTVPASA
 184 CLTVPASA

CLTvPaSA

FIGURE 7I

<u>SEQ</u>	<u>ID NO:</u>	<u>ISOLATE</u>
205		SA11
202		SA3
198		SA4
199		SA5
200		SA7
203		SA13
201		SA1
204		SA6

198-205 consensus

1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTn1RPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKrNTNrRPQDVKFPGGGQIVGGVYLLPRRGPrmGVRATRKTSERSQPRGR

MS^TNP^KPQ^RKT^kRNTN^rRPQDV^KFPGGG^QIVGGV^YLLPRRG^PRI^GVRAT^RKT^SERSQ^PPR^R

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
205	SA11
202	SA3
198	SA4
199	SA5
200	SA7
203	SA13
201	SA1
204	SA6

198-205 consensus

```

62 RQIPKARQPTGRSWGQPGYPWPfYANEGlgWAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
62 RQIPKARQPTGRSWGQPGYPWPPLYANEGLeWAGWLLSPRGSRPgWGPNDPRRKSrNLGKV
62 RQIPKARQPTGRSWGQPGYPWPPLYANEGlgWAGWLLSPRGSRPnWGPNDPRRKSrNLGKV
62 RQIPKARQPTGRSWGQPGYPWPPLYANEGlgWAGWLLSPRGSRPnWGPNDPRRKSrNLGKV
62 RQIPKARQPTGRSWGQPGYPWPPLYANEGlgWAGWLLSPRGSRPnWGPNDPRRKSrNLGKV
62 RQIPKARQPTGRSWGQPGYPWPPLYANEGlgWAGWLLSPRGSRPnWGPNDPRRKSrNLGKV
62 RQIPKARQPTGRSWGQPGYPWPPLYANEGlgWAGWLLSPRGSRPnWGPNDPRRKSrNLGKV
62 RQIPKARQsaGRSWGQPGYPWPPLYANEGlgWAGWLLSPRGSRPnWGPNDPRRKSrNLGKV

```

RQPIPKARQptGRSWGQPGYPWPlYANEGLgWAGWLLSPRGSRpWGPNDPRRkSRNLGKV

<u>SEO ID NO:</u>	<u>ISOLATE</u>
205	SA11
202	SA3
198	SA4
199	SA5
200	SA7
203	SA13
201	SA1
204	SA6

198-205 consensus

[illegible]

IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFiLALLS

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
205	SA11
202	SA3
198	SA4
199	SA5
200	SA7
203	SA13
201	SA1
204	SA6

198-205 consensus

184 CLTVPATA
184 CLTVPASA
184 CLTVPASA
184 CLTVPASA
184 CLTVPASA
184 CLTVPtSA
184 CLiiPASA
184 CLtvPASA

CLtvPasA

FIGURE 7J

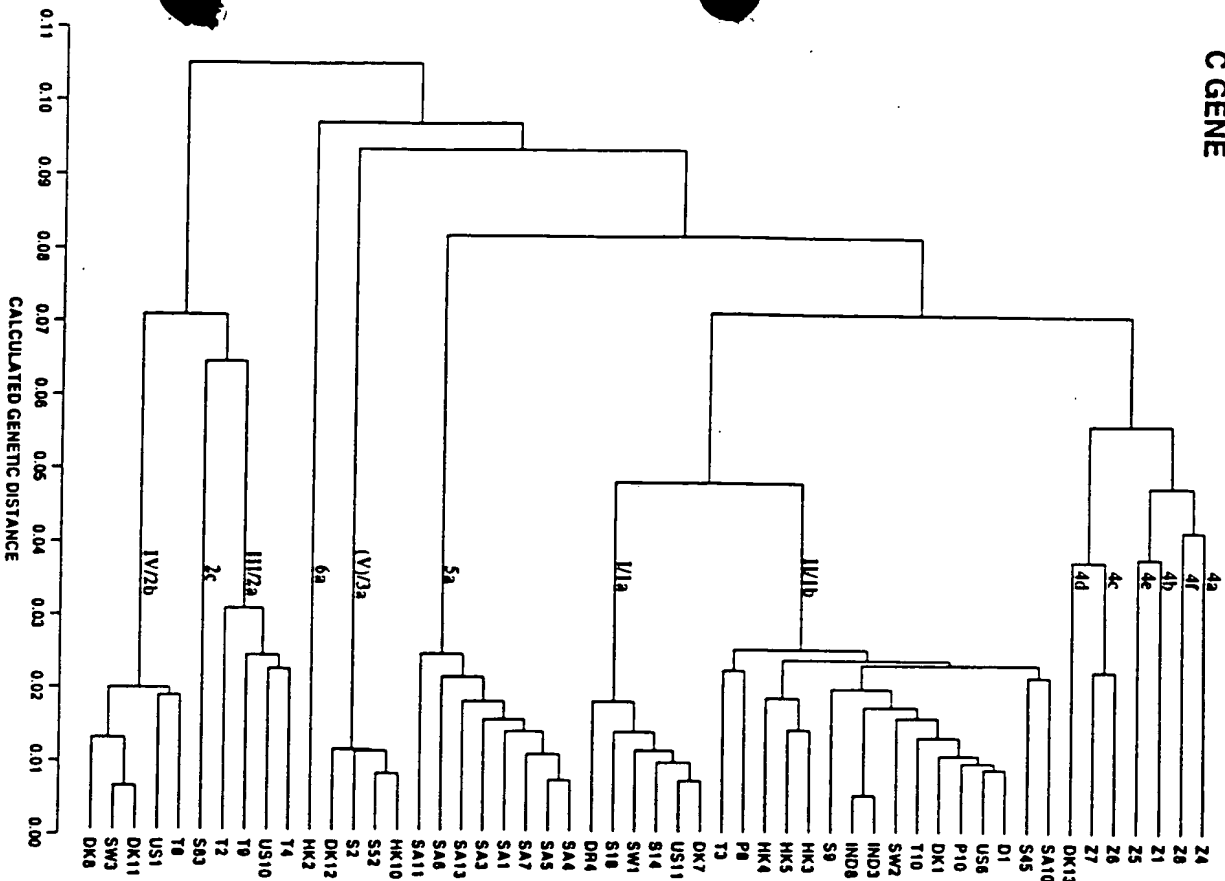
SEQ ID NO:	Genotype	
155-206	cons.	1 MSTnPKPQKTKRNTnRPQDVKFPGGQIVGGVYLLPRRGPRlGVRatRKtSERSQPRRRQPIPKaRtpeGrSWaqpGypWPlyGnEGcgWAGW
155-176	type 1	MSTnPKPQKTKRNTnRRPQDVKFPGGQIVGGVYLLPRRGPRlGVRatRKtSERSQPRRRQPIPKaRtpeGrSWaqpGypWPlyGnEGcgWAGW
177-186	type 2	MSTnPKPQKTKRNTnRRPQDVKFPGGQIVGGVYLLPRRGPRlGVRatRKtSERSQPRRRQPIPKaRtpeGrSWaqpGypWPlyGnEGcgWAGW
187-190	type 3	MSTnPKPQKTKRNTnRRPQDVKFPGGQIVGGVYLLPRRGPRlGVRatRKtSERSQPRRRQPIPKaRtpeGrSWaqpGypWPlyGnEGcgWAGW
191-197	type 4	MSTnPKPQKTKRNTnRRPQDVKFPGGQIVGGVYLLPRRGPRlGVRatRKtSERSQPRRRQPIPKaRtpeGrSWaqpGypWPlyGnEGcgWAGW
198-205	type 5	MSTnPKPQKTKRNTnRRPQDVKFPGGQIVGGVYLLPRRGPRlGVRatRKtSERSQPRRRQPIPKaRtpeGrSWaqpGypWPlyGnEGcgWAGW
206	type 6	MSTnPKPQKTKRNTnRRPQDVKFPGGQIVGGVYLLPRRGPRlGVRatRKtSERSQPRRRQPIPKaRtpeGrSWaqpGypWPlyGnEGcgWAGW
155-206	cons.	97 LLSPrGSRPaWGptDPrrrSRNlgkVIDTlTCgfADLMGYiPlVGaPlGGvArAlAHGVRvLEdGvNyATGNIpGcSFsIFlLALlSCLtvpAaA
155-176	type 1	LLSPrGSRPaWGptDPrrrSRNlgkVIDTlTCGFADLMGYiPlVGaPlGGvArAlAHGVRvLEdGvNyATGNIpGcSFsIFlLALlSCLtvpAaA
177-186	type 2	LLSPrGSRPaWGptDPrrrSRNlgkVIDTlTCGFADLMGYiPlVGaPlGGvArAlAHGVRvLEdGvNyATGNIpGcSFsIFlLALlSCLtvpAaA
187-190	type 3	LLSPrGSRPaWGptDPrrrSRNlgkVIDTlTCGFADLMGYiPlVGaPlGGvArAlAHGVRvLEdGvNyATGNIpGcSFsIFlLALlSCLtvpAaA
191-197	type 4	LLSPrGSRPaWGptDPrrrSRNlgkVIDTlTCGFADLMGYiPlVGaPlGGvArAlAHGVRvLEdGvNyATGNIpGcSFsIFlLALlSCLtvpAaA
198-205	type 5	LLSPrGSRPaWGptDPrrrSRNlgkVIDTlTCGFADLMGYiPlVGaPlGGvArAlAHGVRvLEdGvNyATGNIpGcSFsIFlLALlSCLtvpAaA
206	type 6	LLSPrGSRPaWGptDPrrrSRNlgkVIDTlTCGFADLMGYiPlVGaPlGGvArAlAHGVRvLEdGvNyATGNIpGcSFsIFlLALlSCLtvpAaA

FIGURE 7X

SEQ ID NO:	Genotype	10	20	30	40	50	60	70	80	90
155-160	I/1a	MSTNPKPQRKTKRNTNRPQDKVKGPGGQ	VGGVYILPRRCPR	IGVRStKtSERSOPRCRRRP	IPKaRtpeGrSuaop	dyPWP	YgnEGcgWAGW			
161-176	I/1b	---N---K-K---NR-Q-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
177-180	III/2a	---N---K-K---NR-Q-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
181-185	IV/2b	---N---K-K---NR-Q-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
186	2c	---N---K-K---NR-Q-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
187-190	(V)/3a	---L---K-K---NR-Q-V---	---V---L---AT-T---	---V---L---AT-T---	---V---L---AT-T---	---V---L---AT-T---	---V---L---AT-T---	---V---L---AT-T---	---V---L---AT-T---	---V---L---AT-T---
191	4a	---N---K-K---NR-M-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
193	4b	---N---K-K---NR-M-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
195	4c	---N---K-K---NR-M-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
197	4d	---N---K-K---NR-M-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
198-205	4e	---N---K-K---NR-M-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
199	4f	---N---K-K---NR-M-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
206	5a	---N---K-K---NR-Q-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---
	6a	---L---K-K---NR-T-V---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---	---L---L---AT-T---

SEQ ID NO:	Genotype	100	110	120	130	140	150	160	170	180	190
155-160	I/1a	LLSPGSRPaWGptOPRRrSRNIGKVIDT	ITCGfADLMGYIP	IVGaP	IGGVARALANGVRV	IEDGWNATGN	IPGCSFSIFILAL	ISCLtVpasa			
161-176	I/1b	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
177-180	III/2a	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
181-185	IV/2b	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
186	2c	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
187-190	(V)/3a	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
191	4a	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
193	4b	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
195	4c	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
197	4d	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
198-205	4e	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
199	4f	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
206	5a	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---
	6a	---R-R-S-Pt---RR---L-K---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---	---L-K---L-GF---

C GENE



E1 GENE

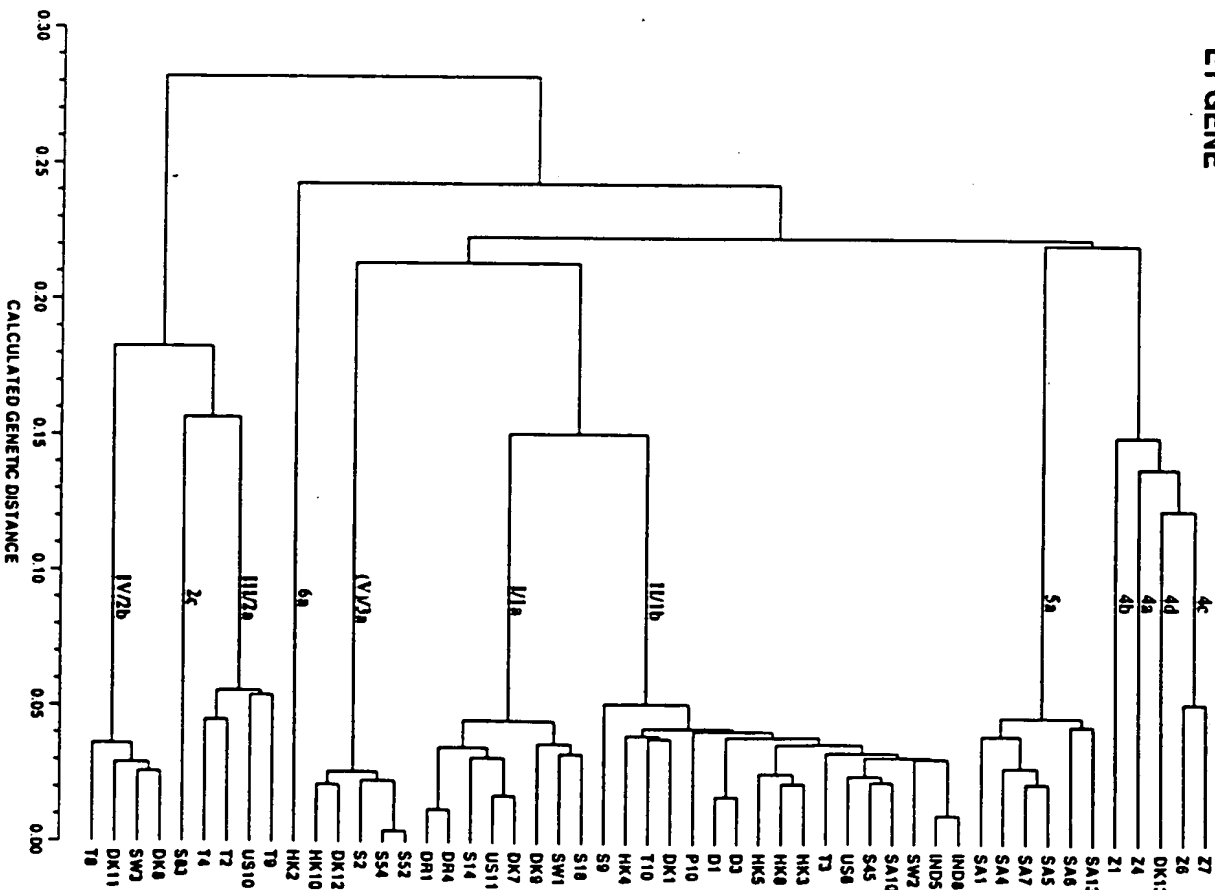


FIGURE 8

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